

PCTWORLD INTELLECTUAL PROPERTY
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER

WO 9608582A2

| | | | |
|--|--|--|---|
| (51) International Patent Classification ⁶ : C12Q 1/68, C12N 15/11 // C12R 1/68 | | A2 | (11) International Publication Number: WO 96/08582 |
| | | | (43) International Publication Date: 21 March 1996 (21.03.96) |
| (21) International Application Number: PCT/CA95/00528 | | (81) Designated States: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT, UA, UG, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, MW, SD, SZ, UG). | |
| (22) International Filing Date: 12 September 1995 (12.09.95) | | Published Without international search report and to be republished upon receipt of that report. | |
| (30) Priority Data: 08/304,732 12 September 1994 (12.09.94) US | | | |
| (71)(72) Applicants and Inventors: BERGERON, Michel, G. [CA/CA]; 2069 Brûlard Street, Sillery, Quebec G1T 1G2 (CA). OUELLETTE, Marc [CA/CA]; 975 Casot Street, Quebec, Quebec G1S 2Y2 (CA). ROY, Paul, H. [US/CA]; 28 Charles Garnier Street, Loretteville, Quebec G2A 2X8 (CA). | | | |
| (74) Agents: DUBUC, Jean, H. et al.; Goudreau Gage Dubuc & Martineau Walker, 3400 Stock Exchange Tower, Victoria Square, P.O. Box 242, Montreal, Quebec H4Z 1E9 (CA). | | | |
| (54) Title: SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN MICROBIOLOGY LABORATORIES | | | |
| (57) Abstract | | | |
| <p>The present invention relates to DNA-based methods for universal bacterial detection, for specific detection of the <i>pneumoniae</i>, <i>Pseudomonas aeruginosa</i>, <i>Proteus mirabilis</i>, <i>Streptococcus pneumoniae</i>, <i>Staphylococcus aureus</i>, <i>Staphylococcus epidermidis</i>, <i>Enterococcus faecalis</i>, <i>Staphylococcus saprophyticus</i>, <i>Streptococcus pyogenes</i>, <i>Haemophilus influenzae</i> and <i>Moraxella catarrhalis</i> as well as for specific detection of commonly encountered and clinically relevant bacterial antibiotic resistance genes directly from clinical specimens or, alternatively, from a bacterial colony. The above bacterial species can account for as much as 80 % of bacterial pathogens isolated in routine microbiology laboratories. The core of this invention consists primarily of the DNA sequences from all species-specific genomic DNA fragments selected by hybridization from genomic libraries or, alternatively, selected from data banks as well as any oligonucleotide sequences derived from these sequences which can be used as probes or amplification primers for PCR or any other nucleic acid amplification methods. This invention also includes DNA sequences from the selected clinically relevant antibiotic resistance genes.</p> | | | |

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

| | | | | | |
|----|--------------------------|----|--|----|--------------------------|
| AT | Austria | GB | United Kingdom | MR | Mauritania |
| AU | Australia | GE | Georgia | MW | Malawi |
| BB | Barbados | GN | Guinea | NE | Niger |
| BE | Belgium | GR | Greece | NL | Netherlands |
| BF | Burkina Faso | HU | Hungary | NO | Norway |
| BG | Bulgaria | IE | Ireland | NZ | New Zealand |
| BJ | Benin | IT | Italy | PL | Poland |
| BR | Brazil | JP | Japan | PT | Portugal |
| BY | Belarus | KE | Kenya | RO | Romania |
| CA | Canada | KG | Kyrgyzstan | RU | Russian Federation |
| CF | Central African Republic | KP | Democratic People's Republic of Korea | SD | Sudan |
| CG | Congo | KR | Republic of Korea | SE | Sweden |
| CH | Switzerland | KZ | Kazakhstan | SI | Slovenia |
| CI | Côte d'Ivoire | LI | Liechtenstein | SK | Slovakia |
| CM | Cameroon | LK | Sri Lanka | SN | Senegal |
| CN | China | LU | Luxembourg | TD | Chad |
| CS | Czechoslovakia | LV | Latvia | TG | Togo |
| CZ | Czech Republic | MC | Monaco | TJ | Tajikistan |
| DE | Germany | MD | Republic of Moldova | TT | Trinidad and Tobago |
| DK | Denmark | MG | Madagascar | UA | Ukraine |
| ES | Spain | ML | Mali | US | United States of America |
| FI | Finland | MN | Mongolia | UZ | Uzbekistan |
| FR | France | | | VN | Viet Nam |
| GA | Gabon | | | | |

SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION
PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON
BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN
5 MICROBIOLOGY LABORATORIES.

BACKGROUND OF THE INVENTION

Classical identification of bacteria

10 Bacteria are classically identified by their ability to
utilize different substrates as a source of carbon and
nitrogen through the use of biochemical tests such as the
API20E™ system. Susceptibility testing of Gram negative
bacilli has progressed to microdilution tests. Although the
15 API and the microdilution systems are cost-effective, at least
two days are required to obtain preliminary results due to the
necessity of two successive overnight incubations to isolate
and identify the bacteria from the specimen. Some faster
detection methods with sophisticated and expensive apparatus
20 have been developed. For example, the fastest identification
system, the autoSCAN-Walk-Away™ system identifies both Gram
negative and Gram positive from isolated bacterial colonies in
2 hours and susceptibility patterns to antibiotics in only 7
hours. However, this system has an unacceptable margin of
25 error, especially with bacterial species other than
Enterobacteriaceae (York et al., 1992. J. Clin. Microbiol.
30:2903-2910). Nevertheless, even this fastest method requires
primary isolation of the bacteria as a pure culture, a process
which takes at least 18 hours if there is a pure culture or 2
30 to 3 days if there is a mixed culture.

Urine specimens

A large proportion (40-50%) of specimens received in
routine diagnostic microbiology laboratories for bacterial
35 identification are urine specimens (Pezzlo, 1988, Clin.
Microbiol. Rev. 1:268-280). Urinary tract infections (UTI) are
extremely common and affect up to 20% of women and account for

SUBSTITUTE SHEET

extensive morbidity and increased mortality among hospitalized patients (Johnson and Stamm, 1989; Ann. Intern. Med. 111:906-917). UTI are usually of bacterial etiology and require antimicrobial therapy. The Gram negative bacillus *Escherichia coli* is by far the most prevalent urinary pathogen and accounts for 50 to 60 % of UTI (Pezzlo, 1988, op. cit.). The prevalence for bacterial pathogens isolated from urine specimens observed recently at the "Centre Hospitalier de l'Université Laval (CHUL)" is given in Tables 1 and 2.

10

Conventional pathogen identification in urine specimens. The search for pathogens in urine specimens is so preponderant in the routine microbiology laboratory that a myriad of tests have been developed. The gold standard is still the classical semi-quantitative plate culture method in which a calibrated loop of urine is streaked on plates and incubated for 18-24 hours. Colonies are then counted to determine the total number of colony forming units (CFU) per liter of urine. A bacterial UTI is normally associated with a bacterial count of $\geq 10^7$ CFU/L in urine. However, infections with less than 10^7 CFU/L in urine are possible, particularly in patients with a high incidence of diseases or those catheterized (Stark and Maki, 1984, N. Engl. J. Med. 311:560-564). Importantly, close to 80% of urine specimens tested are considered negative ($< 10^7$ CFU/L; Table 3).

25

Accurate and rapid urine screening methods for bacterial pathogens would allow a faster identification of negative results and a more efficient clinical investigation of the patient. Several rapid identification methods (Uriscreen™, UTIscreen™, Flash Track™ DNA probes and others) were recently compared to slower standard biochemical methods which are based on culture of the bacterial pathogens. Although much faster, these rapid tests showed low sensitivities and specificities as well as a high number of false negative and false positive results (Koenig et al., 1992. J. Clin. Microbiol. 30:342-345; Pezzlo et al., 1992. J. Clin. Microbiol. 30:640-684).

35

Urine specimens found positive by culture are further characterized using standard biochemical tests to identify the bacterial pathogen and are also tested for susceptibility to antibiotics.

5

Any clinical specimens

As with urine specimen which was used here as an example, our probes and amplification primers are also applicable to any other clinical specimens. The DNA-based tests proposed in this invention are superior to standard methods currently used for routine diagnosis in terms of rapidity and accuracy. While a high percentage of urine specimens are negative, in many other clinical specimens more than 95% of cultures are negative (Table 4). These data further support the use of universal probes to screen out the negative clinical specimens. Clinical specimens from organisms other than humans (e.g. other primates, mammals, farm animals or live stocks) may also be used.

20 Towards the development of rapid DNA-based diagnostic tests

A rapid diagnostic test should have a significant impact on the management of infections. For the identification of pathogens and antibiotic resistance genes in clinical samples, DNA probe and DNA amplification technologies offer several advantages over conventional methods. There is no need for subculturing, hence the organism can be detected directly in clinical samples thereby reducing the costs and time associated with isolation of pathogens. DNA-based technologies have proven to be extremely useful for specific applications in the clinical microbiology laboratory. For example, kits for the detection of fastidious organisms based on the use of hybridization probes or DNA amplification for the direct detection of pathogens in clinical specimens are commercially available (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

SUBSTITUTE SHEET

The present invention is an advantageous alternative to the conventional culture identification methods used in hospital clinical microbiology laboratories and in private clinics for routine diagnosis. Besides being much faster, DNA-based diagnostic tests are more accurate than standard biochemical tests presently used for diagnosis because the bacterial genotype (e.g. DNA level) is more stable than the bacterial phenotype (e.g. biochemical properties). The originality of this invention is that genomic DNA fragments (size of at least 100 base pairs) specific for 12 species of commonly encountered bacterial pathogens were selected from genomic libraries or from data banks. Amplification primers or oligonucleotide probes (both less than 100 nucleotides in length) which are both derived from the sequence of species-specific DNA fragments identified by hybridization from genomic libraries or from selected data bank sequences are used as a basis to develop diagnostic tests. Oligonucleotide primers and probes for the detection of commonly encountered and clinically important bacterial resistance genes are also included. For example, Annexes I and II present a list of suitable oligonucleotide probes and PCR primers which were all derived from the species-specific DNA fragments selected from genomic libraries or from data bank sequences. It is clear to the individual skilled in the art that oligonucleotide sequences appropriate for the specific detection of the above bacterial species other than those listed in Annexes 1 and 2 may be derived from the species-specific fragments or from the selected data bank sequences. For example, the oligonucleotides may be shorter or longer than the ones we have chosen and may be selected anywhere else in the identified species-specific sequences or selected data bank sequences. Alternatively, the oligonucleotides may be designed for use in amplification methods other than PCR. Consequently, the core of this invention is the identification of species-specific genomic DNA fragments from bacterial genomic DNA libraries and the selection of genomic DNA fragments from data bank sequences which are used as a source of species-specific

and ubiquitous oligonucleotides. Although the selection of oligonucleotides suitable for diagnostic purposes from the sequence of the species-specific fragments or from the selected data bank sequences requires much effort it is quite possible for the individual skilled in the art to derive from our fragments or selected data bank sequences suitable oligonucleotides which are different from the ones we have selected and tested as examples (Annexes I and II).

Others have developed DNA-based tests for the detection and identification of some of the bacterial pathogens for which we have identified species-specific sequences (PCT patent application Serial No. WO 93/03186). However, their strategy was based on the amplification of the highly conserved 16S rRNA gene followed by hybridization with internal species-specific oligonucleotides. The strategy from this invention is much simpler and more rapid because it allows the direct amplification of species-specific targets using oligonucleotides derived from the species-specific bacterial genomic DNA fragments.

Since a high percentage of clinical specimens are negative, oligonucleotide primers and probes were selected from the highly conserved 16S or 23S rRNA genes to detect all bacterial pathogens possibly encountered in clinical specimens in order to determine whether a clinical specimen is infected or not. This strategy allows rapid screening out of the numerous negative clinical specimens submitted for bacteriological testing.

We are also developing other DNA-based tests, to be performed simultaneously with bacterial identification, to determine rapidly the putative bacterial susceptibility to antibiotics by targeting commonly encountered and clinically relevant bacterial resistance genes. Although the sequences from the selected antibiotic resistance genes are available and have been used to develop DNA-based tests for their detection (Ehrlich and Greenberg, 1994. PCR-based Diagnostics in Infectious Diseases, Blackwell Scientific Publications, Boston, Massachusetts; Persing et al, 1993. Diagnostic

SUBSTITUTE SHEET

Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.), our approach is innovative as it represents major improvements over current "gold standard" diagnostic methods based on culture of the bacteria because it allows the rapid identification of the presence of a specific bacterial pathogen and evaluation of its susceptibility to antibiotics directly from the clinical specimens within one hour.

We believe that the rapid and simple diagnostic tests not based on cultivation of the bacteria that we are developing will gradually replace the slow conventional bacterial identification methods presently used in hospital clinical microbiology laboratories and in private clinics. In our opinion, these rapid DNA-based diagnostic tests for severe and common bacterial pathogens and antibiotic resistance will (i) save lives by optimizing treatment, (ii) diminish antibiotic resistance by reducing the use of broad spectrum antibiotics and (iii) decrease overall health costs by preventing or shortening hospitalizations.

20

SUMMARY OF THE INVENTION

In accordance with the present invention, there is provided sequence from genomic DNA fragments (size of at least 100 base pairs and all described in the sequence listing) selected either by hybridization from genomic libraries or from data banks and which are specific for the detection of commonly encountered bacterial pathogens (i.e. *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Enterococcus faecalis*, *Staphylococcus saprophyticus*, *Streptococcus pyogenes*, *Haemophilus influenzae* and *Moraxella catarrhalis*) in clinical specimens. These bacterial species are associated with approximately 90% of urinary tract infections and with a high percentage of other severe infections including septicemia, meningitis, pneumonia, intraabdominal infections, skin infections and many other severe respiratory tract infections. Overall, the above bacterial species may account for up to 80% of bacterial pathogens isolated in routine microbiology laboratories.

Synthetic oligonucleotides for hybridization (probes) or DNA amplification (primers) were derived from the above species-specific DNA fragments (ranging in sizes from 0.25 to 5.0 kilobase pairs (kbp)) or from selected data bank sequences (GenBank and EMBL). Bacterial species for which some of the oligonucleotide probes and amplification primers were derived from selected data bank sequences are *Escherichia coli*, *Enterococcus faecalis*, *Streptococcus pyogenes* and *Pseudomonas aeruginosa*. The person skilled in the art understands that the important innovation in this invention is the identification of the species-specific DNA fragments selected either from bacterial genomic libraries by hybridization or from data bank sequences. The selection of oligonucleotides from these fragments suitable for diagnostic purposes is also innovative. Specific and ubiquitous oligonucleotides different from the

SUBSTITUTE SHEET

ones tested in the practice are considered as embodiments of the present invention.

The development of hybridization (with either fragment or oligonucleotide probes) or of DNA amplification protocols for the detection of pathogens from clinical specimens renders possible a very rapid bacterial identification. This will greatly reduce the time currently required for the identification of pathogens in the clinical laboratory since these technologies can be applied for bacterial detection and identification directly from clinical specimens with minimum pretreatment of any biological specimens to release bacterial DNA. In addition to being 100% specific, probes and amplification primers allow identification of the bacterial species directly from clinical specimens or, alternatively, from an isolated colony. DNA amplification assays have the added advantages of being faster and more sensitive than hybridization assays, since they allow rapid and exponential in vitro replication of the target segment of DNA from the bacterial genome. Universal probes and amplification primers selected from the 16S or 23S rRNA genes highly conserved among bacteria, which permit the detection of any bacterial pathogens, will serve as a procedure to screen out the numerous negative clinical specimens received in diagnostic laboratories. The use of oligonucleotide probes or primers complementary to characterized bacterial genes encoding resistance to antibiotics to identify commonly encountered and clinically important resistance genes is also under the scope of this invention.

30

DETAILED DESCRIPTION OF THE INVENTION

Development of species-specific DNA probes

DNA fragment probes were developed for the following bacterial species: *Escherichia coli*, *Kl bsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus epidermidis*,

SUBSTITUTE SHEET

Staphylococcus saprophyticus, *Haemophilus influenzae* and *Moraxella catarrhalis*. (For *Enterococcus faecalis* and *Streptococcus pyogenes*, oligonucleotide sequences were exclusively derived from selected data bank sequences). These species-specific fragments were selected from bacterial genomic libraries by hybridization to DNA from a variety of Gram positive and Gram negative bacterial species (Table 5).

The chromosomal DNA from each bacterial species for which probes were sought was isolated using standard methods. DNA was digested with a frequently cutting restriction enzyme such as *Sau3AI* and then ligated into the bacterial plasmid vector pGEM3Zf (Promega) linearized by appropriate restriction endonuclease digestion. Recombinant plasmids were then used to transform competent *E. coli* strain DH5 α thereby yielding a genomic library. The plasmid content of the transformed bacterial cells was analyzed using standard methods. DNA fragments of target bacteria ranging in size from 0.25 to 5.0 kilobase pairs (kbp) were cut out from the vector by digestion of the recombinant plasmid with various restriction endonucleases. The insert was separated from the vector by agarose gel electrophoresis and purified in low melting point agarose gels. Each of the purified fragments of bacterial genomic DNA was then used as a probe for specificity tests.

For each given species, the gel-purified restriction fragments of unknown coding potential were labeled with the radioactive nucleotide α -³²P(dATP) which was incorporated into the DNA fragment by the random priming labeling reaction. Non-radioactive modified nucleotides could also be incorporated into the DNA by this method to serve as a label.

Each DNA fragment probe (i.e. a segment of bacterial genomic DNA of at least 100 bp in length cut out from clones randomly selected from the genomic library) was then tested for its specificity by hybridization to DNAs from a variety of bacterial species (Table 5). The double-stranded labeled DNA probe was heat-denatured to yield labeled single-stranded DNA which could then hybridize to any single-stranded target DNA fixed onto a solid support or in solution. The target DNAs

SUBSTITUTE SHEET

consisted of total cellular DNA from an array of bacterial species found in clinical samples (Table 5). Each target DNA was released from the bacterial cells and denatured by conventional methods and then irreversibly fixed onto a solid support (e.g. nylon or nitrocellulose membranes) or free in solution. The fixed single-stranded target DNAs were then hybridized with the single-stranded probe. Pre-hybridization, hybridization and post-hybridization conditions were as follows: (i) Pre-hybridization; in 1 M NaCl + 10% dextran sulfate + 1% SDS (sodium dodecyl sulfate) + 100 µg/ml salmon sperm DNA at 65°C for 15 min. (ii) Hybridization; in fresh pre-hybridization solution containing the labeled probe at 65°C overnight. (iii) Post-hybridization; washes twice in 3X SSC containing 1% SDS (1X SSC is 0.15M NaCl, 0.015M NaCitrate) and twice in 0.1 X SSC containing 0.1% SDS; all washes were at 65°C for 15 min. Autoradiography of washed filters allowed the detection of selectively hybridized probes. Hybridization of the probe to a specific target DNA indicated a high degree of similarity between the nucleotide sequence of these two DNAs.

Species-specific DNA fragments selected from various bacterial genomic libraries ranging in size from 0.25 to 5.0 kbp were isolated for 10 common bacterial pathogens (Table 6) based on hybridization to chromosomal DNAs from a variety of bacteria performed as described above. All of the bacterial species tested (66 species listed in Table 5) were likely to be pathogens associated with common infections or potential contaminants which can be isolated from clinical specimens. A DNA fragment probe was considered specific only when it hybridized solely to the pathogen from which it was isolated.

DNA fragment probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes recognized most isolates of the target species) by hybridization to bacterial DNAs from approximately 10 to 80 clinical isolates of the species of interest (Table 6). The DNAs were denatured, fixed onto nylon membranes and hybridized as described above.

Sequencing of the species-specific fragment probes

The nucleotide sequence of the totality or of a portion of the species-specific DNA fragments isolated (Table 6) was determined using the dideoxynucleotide termination sequencing method which was performed using Sequenase (USB Biochemicals) or T7 DNA polymerase (Pharmacia). These nucleotide sequences are shown in the sequence listing. Alternatively, sequences selected from data banks (GenBank and EMBL) were used as sources of oligonucleotides for diagnostic purposes for *Escherichia coli*, *Enterococcus faecalis*, *Streptococcus pyogenes* and *Pseudomonas aeruginosa*. For this strategy, an array of suitable oligonucleotide primers or probes derived from a variety of genomic DNA fragments (size of more than 100 bp) selected from data banks was tested for their specificity and ubiquity in PCR and hybridization assays as described later. It is important to note that the data bank sequences were selected based on their potential of being species-specific according to available sequence information. Only data bank sequences from which species-specific oligonucleotides could be derived are included in this invention.

Oligonucleotide probes and amplification primers derived from species-specific fragments selected from the genomic libraries or from data bank sequences were synthesized using an automated DNA synthesizer (Millipore). Prior to synthesis, all oligonucleotides (probes for hybridization and primers for DNA amplification) were evaluated for their suitability for hybridization or DNA amplification by polymerase chain reaction (PCR) by computer analysis using standard programs (e.g. Genetics Computer Group (GCG) and OligoTM 4.0 (National Biosciences)). The potential suitability of the PCR primer pairs was also evaluated prior to the synthesis by verifying the absence of unwanted features such as long stretches of one nucleotide, a high proportion of G or C residues at the 3' end and a 3'-terminal T residue (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

SUBSTITUTE SHEET

Hybridization with oligonucleotide probes

In hybridization experiments, oligonucleotides (size less than 100 nucleotides) have some advantages over DNA fragment probes for the detection of bacteria such as ease of preparation in large quantities, consistency in results from batch to batch and chemical stability. Briefly, for the hybridizations, oligonucleotides were 5' end-labeled with the radionucleotide $\gamma^{32}\text{P}(\text{ATP})$ using T4 polynucleotide kinase (Pharmacia). The unincorporated radionucleotide was removed by passing the labeled single-stranded oligonucleotide through a Sephadex G50 column. Alternatively, oligonucleotides were labeled with biotin, either enzymatically at their 3' ends or incorporated directly during synthesis at their 5' ends, or with digoxigenin. It will be appreciated by the person skilled in the art that labeling means other than the three above labels may be used.

The target DNA was denatured, fixed onto a solid support and hybridized as previously described for the DNA fragment probes. Conditions for pre-hybridization and hybridization were as described earlier. Post-hybridization washing conditions were as follows: twice in 3X SSC containing 1% SDS, twice in 2X SSC containing 1% SDS and twice in 1X SSC containing 1% SDS (all of these washes were at 65°C for 15 min), and a final wash in 0.1X SSC containing 1% SDS at 25°C for 15 min. For probes labeled with radioactive labels the detection of hybrids was by autoradiography as described earlier. For non-radioactive labels detection may be colorimetric or by chemiluminescence.

The oligonucleotide probes may be derived from either strand of the duplex DNA. The probes may consist of the bases A, G, C, or T or analogs. The probes may be of any suitable length and may be selected anywhere within the species-specific genomic DNA fragments selected from the genomic libraries or from data bank sequences.

SUBSTITUTE SHEET

DNA amplification

For DNA amplification by the widely used PCR (polymerase chain reaction) method, primer pairs were derived either from the sequenced species-specific DNA fragments or from data bank sequences or, alternatively, were shortened versions of oligonucleotide probes. Prior to synthesis, the potential primer pairs were analyzed by using the program Oligo™ 4.0 (National Biosciences) to verify that they are likely candidates for PCR amplifications.

During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the denatured double-stranded target DNA from the bacterial genome are used to amplify exponentially in vitro the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and synthesis of new targets at each cycle (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). Briefly, the PCR protocols were as follows. Clinical specimens or bacterial colonies were added directly to the 50 µL PCR reaction mixtures containing 50 mM KCl, 10 mM Tris-HCl pH 8.3, 2.5 mM MgCl₂, 0.4 µM of each of the two primers, 200 µM of each of the four dNTPs and 1.25 Units of Taq DNA polymerase (Perkin Elmer). PCR reactions were then subjected to thermal cycling (3 min at 95°C followed by 30 cycles of 1 second at 95°C and 1 second at 55°C) using a Perkin Elmer 480™ thermal cycler and subsequently analyzed by standard ethidium bromide-stained agarose gel electrophoresis. It is clear that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be used. Such methods may be based on the detection of fluorescence after amplification (e.g. TaqMan™ system from Perkin Elmer or Amplisensor™ from Biotronics) or liquid hybridization with an oligonucleotide probe binding to internal sequences of the specific amplification product. These novel probes can be generated from our species-specific fragment probes. Methods based on the detection of fluorescence are particularly promising for

SUBSTITUTE SHEET

utilization in routine diagnosis as they are, very rapid and quantitative and can be automated.

To assure PCR efficiency, glycerol or dimethyl sulfoxide (DMSO) or other related solvents, can be used to increase the sensitivity of the PCR and to overcome problems associated with the amplification of target with a high GC content or with strong secondary structures. The concentration ranges for glycerol and DMSO are 5-15% (v/v) and 3-10% (v/v), respectively. For the PCR reaction mixture, the concentration ranges for the amplification primers and the $MgCl_2$ are 0.1-1.0 μM and 1.5-3.5 mM, respectively. Modifications of the standard PCR protocol using external and nested primers (i.e. nested PCR) or using more than one primer pair (i.e. multiplex PCR) may also be used (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). For more details about the PCR protocols and amplicon detection methods see examples 7 and 8.

The person skilled in the art of DNA amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), transcription-based amplification systems (TAS), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA) and branched DNA (bDNA) (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any rapid nucleic acid amplification methods or any other procedures which may be used to increase rapidity and sensitivity of the tests. Any oligonucleotides suitable for the amplification of nucleic acid by approaches other than PCR and derived from the species-specific fragments and from selected antibiotic resistance gene sequences included in this document are also under the scope of this invention.

SUBSTITUTE SHEET

Specificity and ubiquity tests for oligonucleotide probes and primers

5 The specificity of oligonucleotide probes, derived either from the sequenced species-specific fragments or from data bank sequences, was tested by hybridization to DNAs from the array of bacterial species listed in Table 5 as previously described. Oligonucleotides found to be specific were subsequently tested for their ubiquity by hybridization to bacterial DNAs from approximately 80 isolates of the target species as described for fragment probes. Probes were considered ubiquitous when they hybridized specifically with the DNA from at least 80% of the isolates. Results for specificity and ubiquity tests with the oligonucleotide probes are summarized in Table 6. The specificity and ubiquity of the amplification primer pairs were tested directly from cultures (see example 7) of the same bacterial strains. For specificity and ubiquity tests, PCR assays were performed directly from bacterial colonies of approximately 80 isolates of the target species. Results are summarized in Table 7. All specific and ubiquitous oligonucleotide probes and amplification primers for each of the 12 bacterial species investigated are listed in Annexes I and II, respectively. Divergence in the sequenced DNA fragments can occur and, insofar as the divergence of these sequences or a part thereof does not affect the specificity of the probes or amplification primers, variant bacterial DNA is under the scope of this invention.

Universal bacterial detection

In the routine microbiology laboratory a high percentage of clinical specimens sent for bacterial identification is negative (Table 4). For example, over a 2 year period, around 5 80% of urine specimens received by the laboratory at the "Centre Hospitalier de l'Université Laval (CHUL)" were negative (i.e. $<10^7$ CFU/L) (Table 3). Testing clinical samples with universal probes or universal amplification primers to detect the presence of bacteria prior to specific 10 identification and screen out the numerous negative specimens is thus useful as it saves costs and may rapidly orient the clinical management of the patients. Several oligonucleotides and amplification primers were therefore synthesized from highly conserved portions of bacterial 16S or 23S ribosomal 15 RNA gene sequences available in data banks (Annexes III and IV). In hybridization tests, a pool of seven oligonucleotides (Annex I; Table 6) hybridized strongly to DNA from all bacterial species listed in Table 5. This pool of universal probes labeled with radionucleotides or with any other 20 modified nucleotides is consequently very useful for detection of bacteria in urine samples with a sensitivity range of $\geq 10^7$ CFU/L. These probes can also be applied for bacterial detection in other clinical samples.

Amplification primers also derived from the sequence of 25 highly conserved ribosomal RNA genes were used as an alternative strategy for universal bacterial detection directly from clinical specimens (Annex IV; Table 7). The DNA amplification strategy was developed to increase the sensitivity and the rapidity of the test. This amplification 30 test was ubiquitous since it specifically amplified DNA from 23 different bacterial species encountered in clinical specimens.

Well-conserved bacterial genes other than ribosomal RNA genes could also be good candidates for universal bacterial 35 detection directly from clinical specimens. Such genes may be associated with processes essential for bacterial survival (e.g. protein synthesis, DNA synthesis, cell division or DNA

SUBSTITUTE SHEET

repair) and could therefore be highly conserved during evolution. We are working on these candidate genes to develop new rapid tests for the universal detection of bacteria directly from clinical specimens.

5

Antibiotic resistance genes

Antimicrobial resistance complicates treatment and often leads to therapeutic failures. Furthermore, overuse of antibiotics inevitably leads to the emergence of bacterial resistance. Our goal is to provide the clinicians, within one hour, the needed information to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal bacterial detection and the identification of the presence of a specific pathogen in the positive specimens with DNA-based tests for specific bacterial detection, the clinicians also need timely information about the ability of the bacterial pathogen to resist antibiotic treatments. We feel that the most efficient strategy to evaluate rapidly bacterial resistance to antimicrobials is to detect directly from the clinical specimens the most common and important antibiotic resistance genes (i.e. DNA-based tests for the detection of antibiotic resistance genes). Since the sequence from the most important and common bacterial antibiotic resistance genes are available from data banks, our strategy is to use the sequence from a portion or from the entire gene to design specific oligonucleotides which will be used as a basis for the development of rapid DNA-based tests. The sequence from the bacterial antibiotic resistance genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in the sequence listing. Table 8 summarizes some characteristics of the selected antibiotic resistance genes.

EXAMPLES

The following examples are intended to be illustrative of the various methods and compounds of the invention.

5

EXAMPLE 1:

Isolation and cloning of fragments. Genomic DNAs from *Escherichia coli* strain ATCC 25922, *Klebsiella pneumoniae* strain CK2, *Pseudomonas aeruginosa* strain ATCC 27853, *Proteus mirabilis* strain ATCC 35657, *Streptococcus pneumoniae* strain ATCC 27336, *Staphylococcus aureus* strain ATCC 25923, *Staphylococcus epidermidis* strain ATCC 12228, *Staphylococcus saprophyticus* strain ATCC 15305, *Haemophilus influenzae* reference strain Rd and *Moraxella catarrhalis* strain ATCC 153879 were prepared using standard procedures. It is understood that the bacterial genomic DNA may have been isolated from strains other than the ones mentioned above. (For *Enterococcus faecalis* and *Streptococcus pyogenes* oligonucleotide sequences were derived exclusively from data banks). Each DNA was digested with a restriction enzyme which frequently cuts DNA such as *Sau3AI*. The resulting DNA fragments were ligated into a plasmid vector (pGEM3Zf) to create recombinant plasmids and transformed into competent *E. coli* cells (DH5 α). It is understood that the vectors and corresponding competent cells should not be limited to the ones herein above specifically exemplified. The objective of obtaining recombinant plasmids and transformed cells is to provide an easily reproducible source of DNA fragments useful as probes. Therefore, insofar as the inserted fragments are specific and selective for the target bacterial DNA, any recombinant plasmids and corresponding transformed host cells are under the scope of this invention. The plasmid content of the transformed bacterial cells was analyzed using standard methods. DNA fragments from target bacteria ranging in size from 0.25 to 5.0 kbp were cut out from the vector by digestion of the recombinant plasmid with various restriction endonucleases. The insert was separated from the vector by

SUBSTITUTE SHEET

agarose gel electrophoresis and purified in a low melting point agarose gel. Each of the purified fragments was then used for specificity tests.

5 Labeling of DNA fragment probes. The label used was $\alpha^{32}\text{P}(\text{dATP})$, a radioactive nucleotide which can be incorporated enzymatically into a double-stranded DNA molecule. The fragment of interest is first denatured by heating at 95°C for
10 to the strands of the fragments. These primers, once annealed, provide a starting point for synthesis of DNA. DNA polymerase, usually the Klenow fragment, is provided along with the four nucleotides, one of which is radioactive. When the reaction is
15 terminated, the mixture of new DNA molecules is once again denatured to provide radioactive single-stranded DNA molecules (i.e. the probe). As mentioned earlier, other modified nucleotides may be used to label the probes.

20 Specificity and ubiquity tests for the DNA fragment probes. Species-specific DNA fragments ranging in size from 0.25 to 5.0 kbp were isolated for 10 common bacterial pathogens (Table 6) based on hybridization to chromosomal DNAs from a variety of bacteria. Samples of whole cell DNA for each bacterial strain listed in Table 5 were transferred onto a
25 nylon membrane using a dot blot apparatus, washed and denatured before being irreversibly fixed. Hybridization conditions were as described earlier. A DNA fragment probe was considered specific only when it hybridized solely to the pathogen from which it was isolated. Labeled DNA fragments
30 hybridizing specifically only to target bacterial species (i.e. specific) were then tested for their ubiquity by hybridization to DNAs from approximately 10 to 80 isolates of the species of interest as described earlier. The conditions for pre-hybridization, hybridization and post-hybridization
35 washes were as described earlier. After autoradiography (or other detection means appropriate for the non-radioactive label used), the specificity of each individual probe can be

SUBSTITUTE SHEET

determined. Each probe found to be specific (i.e. hybridizing only to the DNA from the bacterial species from which it was isolated) and ubiquitous (i.e. hybridizing to most isolates of the target species) was kept for further experimentations.

5

EXAMPLE 2:

Same as example 1 except that testing of the strains is by colony hybridization. The bacterial strains were inoculated onto a nylon membrane placed on nutrient agar. The membranes were incubated at 37°C for two hours and then bacterial lysis and DNA denaturation were carried out according to standard procedures. DNA hybridization was performed as described earlier.

15 **EXAMPLE 3:**

Same as example 1 except that bacteria were detected directly from clinical samples. Any biological samples were loaded directly onto a dot blot apparatus and cells were lysed *in situ* for bacterial detection. Blood samples should be heparinized in order to avoid coagulation interfering with their convenient loading on a dot blot apparatus.

20 **EXAMPLE 4:**

Nucleotide sequencing of DNA fragments. The nucleotide sequence of the totality or a portion of each fragment found to be specific and ubiquitous (Example 1) was determined using the dideoxynucleotide termination sequencing method (Sanger et al., 1977, Proc. Natl. Acad. Sci. USA. 74:5463-5467). These DNA sequences are shown in the sequence listing.

30 Oligonucleotide probes and amplification primers were selected from these nucleotide sequences, or alternatively, from selected data banks sequences and were then synthesized on an automated Biosearch synthesizer (Millipore™) using phosphoramidite chemistry.

35

Labeling of oligonucleotides. Each oligonucleotide was 5' end-labeled with $\gamma^{32}\text{P}$ -ATP by the T4 polynucleotide kinase

SUBSTITUTE SHEET

(Pharmacia) as described earlier. The label could also be non-radioactive.

Specificity test for oligonucleotide probes. All labeled
5 oligonucleotide probes were tested for their specificity by hybridization to DNAs from a variety of Gram positive and Gram negative bacterial species as described earlier. Species-specific probes were those hybridizing only to DNA from the bacterial species from which it was isolated. Oligonucleotide
10 probes found to be specific were submitted to ubiquity tests as follows.

Ubiquity test for oligonucleotide probes. Specific
oligonucleotide probes were then used in ubiquity tests with
15 approximately 80 strains of the target species. Chromosomal DNAs from the isolates were transferred onto nylon membranes and hybridized with labeled oligonucleotide probes as described for specificity tests. The batteries of approximately 80 isolates constructed for each target species
20 contain reference ATCC strains as well as a variety of clinical isolates obtained from various sources. Ubiquitous probes were those hybridizing to at least 80% of DNAs from the battery of clinical isolates of the target species. Examples of specific and ubiquitous oligonucleotide probes are listed
25 in Annex 1.

EXAMPLE 5:

Same as example 4 except that a pool of specific oligonucleotide probes is used for bacterial identification
30 (i) to increase sensitivity and assure 100% ubiquity or (ii) to identify simultaneously more than one bacterial species. Bacterial identification could be done from isolated colonies or directly from clinical specimens.

35 **EXAMPLE 6:**

PCR amplification. The technique of PCR was used to increase sensitivity and rapidity of the tests. The PCR

SUBSTITUTE SHEET

primers used were often shorter derivatives of the extensive sets of oligonucleotides previously developed for hybridization assays (Table 6). The sets of primers were tested in PCR assays performed directly from a bacterial colony or from a bacterial suspension (see Example 7) to determine their specificity and ubiquity (Table 7). Examples of specific and ubiquitous PCR primer pairs are listed in annex II.

10 Specificity and ubiquity tests for amplification primers.

The specificity of all selected PCR primer pairs was tested against the battery of Gram negative and Gram positive bacteria used to test the oligonucleotide probes (Table 5). Primer pairs found specific for each species were then tested for their ubiquity to ensure that each set of primers could amplify at least 80% of DNAs from a battery of approximately 80 isolates of the target species. The batteries of isolates constructed for each species contain reference ATCC strains and various clinical isolates representative of the clinical diversity for each species.

Standard precautions to avoid false positive PCR results should be taken. Methods to inactivate PCR amplification products such as the inactivation by uracil-N-glycosylase may be used to control PCR carryover.

25

EXAMPLE 7:

Amplification directly from a bacterial colony or suspension. PCR assays were performed either directly from a bacterial colony or from a bacterial suspension, the latter being adjusted to a standard McFarland 0.5 (corresponds to 1.5×10^8 bacteria/mL). In the case of direct amplification from a colony, a portion of the colony was transferred directly to a 50 μ L PCR reaction mixture (containing 50 mM KCl, 10 mM Tris pH 8.3, 2.5 mM $MgCl_2$, 0.4 μ M of each of the two primers, 200 μ M of each of the four dNTPs and 1.25 Unit of Taq DNA polymerase (Perkin Elmer)) using a plastic rod. For the bacterial suspension, 4 μ L of the cell suspension was added to

SUBSTITUTE SHEET

46 μ L of the same PCR reaction mixture. For both strategies, the reaction mixture was overlaid with 50 μ L of mineral oil and PCR amplifications were carried out using an initial denaturation step of 3 min. at 95°C followed by 30 cycles consisting of a 1 second denaturation step at 95°C and of a 1 second annealing step at 55°C in a Perkin Elmer 480™ thermal cycler. PCR amplification products were then analyzed by standard agarose gel (2%) electrophoresis. Amplification products were visualized in agarose gels containing 2.5 μ g/mL of ethidium bromide under UV at 254 nm. The entire PCR assay can be completed in approximately one hour.

Alternatively, amplification from bacterial cultures was performed as described above but using a "hot start" protocol. In that case, an initial reaction mixture containing the target DNA, primers and dNTPs was heated at 85°C prior to the addition of the other components of the PCR reaction mixture. The final concentration of all reagents was as described above. Subsequently, the PCR reactions were submitted to thermal cycling and analysis as described above.

EXAMPLE 8:

Amplification directly from clinical specimens. For amplification from urine specimens, 4 μ L of undiluted or diluted (1:10) urine was added directly to 46 μ L of the above PCR reaction mixture and amplified as described earlier.

To improve bacterial cell lysis and eliminate the PCR inhibitory effects of clinical specimens, samples were routinely diluted in lysis buffer containing detergent(s). Subsequently, the lysate was added directly to the PCR reaction mixture. Heat treatments of the lysates, prior to DNA amplification, using the thermocycler or a microwave oven could also be performed to increase the efficiency of cell lysis.

Our strategy is to develop rapid and simple protocols to eliminate PCR inhibitory effects of clinical specimens and lyse bacterial cells to perform DNA amplification directly from a variety of biological samples. PCR has the advantage of

SUBSTITUTE SHEET

being compatible with crude DNA preparations. For example, blood, cerebrospinal fluid and sera may be used directly in PCR assays after a brief heat treatment. We intend to use such rapid and simple strategies to develop fast protocols for DNA
5 amplification from a variety of clinical specimens.

EXAMPLE 9:

Detection of antibiotic resistance genes. The presence of specific antibiotic resistance genes which are frequently
10 encountered and clinically relevant is identified using the PCR amplification or hybridization protocols described in previous sections. Specific oligonucleotides used as a basis for the DNA-based tests are selected from the antibiotic resistance gene sequences. These tests can be performed either
15 directly from clinical specimens or from a bacterial colony and should complement diagnostic tests for specific bacterial identification.

EXAMPLE 10:

20 Same as examples 7 and 8 except that assays were performed by multiplex PCR (i.e. using several pairs of primers in a single PCR reaction) to (i) reach an ubiquity of 100% for the specific target pathogen or (ii) to detect simultaneously several species of bacterial pathogens.

25 For example, the detection of *Escherichia coli* requires three pairs of PCR primers to assure a ubiquity of 100%. Therefore, a multiplex PCR assay (using the "hot-start" protocol (Example 7)) with those three primer pairs was developed. This strategy was also used for the other bacterial
30 pathogens for which more than one primer pair was required to reach an ubiquity of 100%.

Multiplex PCR assays could also be used to (i) detect simultaneously several bacterial species or, alternatively, (ii) to simultaneously identify the bacterial pathogen and
35 detect specific antibiotic resistance genes either directly from a clinical specimen or from a bacterial colony.

SUBSTITUTE SHEET

For these applications, amplicon detection methods should be adapted to differentiate the various amplicons produced. Standard agarose gel electrophoresis could be used because it discriminates the amplicons based on their sizes. Another
5 useful strategy for this purpose would be detection using a variety of fluorochromes emitting at different wavelengths which are each coupled with a specific oligonucleotide linked to a fluorescence quencher which is degraded during amplification to release the fluorochrome (e.g. TaqMan™,
10 Perkin Elmer).

EXAMPLE 11:

Detection of amplification products. The person skilled in the art will appreciate that alternatives other than standard
15 agarose gel electrophoresis (Example 7) may be used for the revelation of amplification products. Such methods may be based on the detection of fluorescence after amplification (e.g. Amplisensor™, Biotronics; TaqMan™) or other labels such as biotin (SHARP Signal™ system, Digene Diagnostics).
20 These methods are quantitative and easily automated. One of the amplification primers or an internal oligonucleotide probe specific to the amplicon(s) derived from the species-specific fragment probes is coupled with the fluorochrome or with any other label. Methods based on the detection of fluorescence
25 are particularly suitable for diagnostic tests since they are rapid and flexible as fluorochromes emitting different wavelengths are available (Perkin Elmer).

EXAMPLE 12:

30 Species-specific, universal and antibiotic resistance gene amplification primers can be used in other rapid amplification procedures such as the ligase chain reaction (LCR), transcription-based amplification systems (TAS), self-sustained sequence replication (3SR), nucleic acid sequence-
35 based amplification (NASBA), strand displacement amplification (SDA) and branched DNA (bdNA) or any other methods to increase the sensitivity of the test. Amplifications can be performed

SUBSTITUTE SHEET

from an isolated bacterial colony or directly from clinical specimens. The scope of this invention is therefore not limited to the use of PCR but rather includes the use of any procedures to specifically identify bacterial DNA and which
5 may be used to increase rapidity and sensitivity of the tests.

EXAMPLE 13:

A test kit would contain sets of probes specific for each bacterium as well as a set of universal probes. The kit is
10 provided in the form of test components, consisting of the set of universal probes labeled with non-radioactive labels as well as labeled specific probes for the detection of each bacterium of interest in specific clinical samples. The kit will also include test reagents necessary to perform the pre-
15 hybridization, hybridization, washing steps and hybrid detection. Finally, test components for the detection of known antibiotic resistance genes (or derivatives therefrom) will be included. Of course, the kit will include standard samples to be used as negative and positive controls for each
20 hybridization test.

Components to be included in the kits will be adapted to each specimen type and to detect pathogens commonly encountered in that type of specimen. Reagents for the universal detection of bacteria will also be included. Based
25 on the sites of infection, the following kits for the specific detection of pathogens may be developed:

-A kit for the universal detection of bacterial pathogens from most clinical specimens which contains sets of probes specific for highly conserved regions of the bacterial
30 genomes.

-A kit for the detection of bacterial pathogens retrieved from urine samples, which contains eight specific test components (sets of probes for the detection of *Escherichia coli*, *Enterococcus faecalis*, *Kl bsiella pneumoniae*, *Proteus mirabilis*, *Pseudomonas aeruginosa*, *Staphylococcus saprophyticus*, *Staphylococcus aureus* and *Staphylococcus epidermidis*).

SUBSTITUTE SHEET

-A kit for the detection of respiratory pathogens which contains seven specific test components (sets of probes for detecting *Streptococcus pneumoniae*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Streptococcus pyogenes* and *Staphylococcus aureus*).

-A kit for the detection of pathogens retrieved from blood samples, which contains eleven specific test components (sets of probes for the detection of *Streptococcus pneumoniae*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Proteus mirabilis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Enterococcus faecalis*, *Staphylococcus aureus*, *Streptococcus pyogenes* and *Staphylococcus epidermidis*).

-A kit for the detection of pathogens causing meningitis, which contains four specific test components (sets of probes for the detection of *Haemophilus influenzae*, *Streptococcus pneumoniae*, *Escherichia coli* and *Pseudomonas aeruginosa*).

-A kit for the detection of clinically important antibiotic resistance genes which contains sets of probes for the specific detection of at least one of the 19 following genes associated with bacterial resistance : *bla_{TEM}*, *bla_{ROB}*, *bla_{SHV}*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *mecA*, *vanA*, *vanH*, *vanX*, *satA*, *aacA-aphD*, *vat*, *vga*, *msrA*, *sul* and *int*.

-Other kits adapted for the detection of pathogens from skin, abdominal wound or any other clinically relevant kits will be developed.

EXAMPLE 14:

Same as example 13 except that the test kits contain all reagents and controls to perform DNA amplification assays. Diagnostic kits will be adapted for amplification by PCR (or other amplification methods) performed directly either from clinical specimens or from a bacterial colony. Components required for universal bacterial detection, bacterial identification and antibiotic resistance genes detection will be included.

SUBSTITUTE SHEET

Amplification assays could be performed either in tubes or in microtitration plates having multiple wells. For assays in plates, the wells will be coated with the specific amplification primers and control DNAs and the detection of amplification products will be automated. Reagents and amplification primers for universal bacterial detection will be included in kits for tests performed directly from clinical specimens. Components required for bacterial identification and antibiotic resistance gene detection will be included in kits for testing directly from colonies as well as in kits for testing directly from clinical specimens.

The kits will be adapted for use with each type of specimen as described in example 13 for hybridization-based diagnostic kits.

15

EXAMPLE 15:

It is understood that the use of the probes and amplification primers described in this invention for bacterial detection and identification is not limited to clinical microbiology applications. In fact, we feel that other sectors could also benefit from these new technologies. For example, these tests could be used by industries for quality control of food, water, pharmaceutical products or other products requiring microbiological control. These tests could also be applied to detect and identify bacteria in biological samples from organisms other than humans (e.g. other primates, mammals, farm animals and live stocks). These diagnostic tools could also be very useful for research purposes including clinical trials and epidemiological studies.

30

SUBSTITUTE SHEET

Table 1. Distribution of urinary isolates from positive urine samples ($\geq 10^7$ CFU/L) at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992-1994 period.

| | | % of isolates | | | |
|----|-------------------------------------|--------------------|--------|--------|--------|
| 10 | Organisms | Nov 92 | Apr 93 | Jul 93 | Jan 94 |
| | | n=267 ^a | n=265 | n=238 | n=281 |
| | <i>Escherichia coli</i> | 53.2 | 51.7 | 53.8 | 54.1 |
| | <i>Enterococcus faecalis</i> | 13.8 | 12.4 | 11.7 | 11.4 |
| 15 | <i>Klebsiella pneumoniae</i> | 6.4 | 6.4 | 5.5 | 5.3 |
| | <i>Staphylococcus epidermidis</i> | 7.1 | 7.9 | 3.0 | 6.4 |
| | <i>Proteus mirabilis</i> | 2.6 | 3.4 | 3.8 | 2.5 |
| | <i>Pseudomonas aeruginosa</i> | 3.7 | 3.0 | 5.0 | 2.9 |
| | <i>Staphylococcus saprophyticus</i> | 3.0 | 1.9 | 5.4 | 1.4 |
| 20 | Others ^b | 10.2 | 13.3 | 11.8 | 16.0 |

^a n = total number of isolates for the indicated month.

^b See Table 2.

SUBSTITUTE SHEET

Table 2. Distribution of uncommon^a urinary isolates from positive urine samples ($\geq 10^7$ CFU/L) at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992-1994 period.

| 10 | Organisms ^a | % of isolates | | | |
|----|-----------------------------------|---------------|--------|--------|--------|
| | | Nov 92 | Apr 93 | Jul 93 | Jan 94 |
| | <i>Staphylococcus aureus</i> | 0.4 | 1.1 | 1.3 | 1.4 |
| | <i>Staphylococcus spp.</i> | 2.2 | 4.9 | 1.7 | 6.0 |
| 15 | <i>Micrococcus spp.</i> | 0.0 | 0.0 | 0.4 | 0.7 |
| | <i>Enterococcus faecium</i> | 0.4 | 0.4 | 1.3 | 1.4 |
| | <i>Citrobacter spp.</i> | 1.4 | 0.8 | 0.4 | 0.7 |
| | <i>Enterobacter spp.</i> | 1.5 | 1.1 | 1.3 | 1.4 |
| | <i>Klebsiella oxytoca</i> | 1.1 | 1.5 | 2.5 | 1.8 |
| 20 | <i>Serratia spp.</i> | 0.8 | 0.0 | 0.5 | 0.0 |
| | <i>Proteus spp.</i> | 0.4 | 0.4 | 0.0 | 1.1 |
| | <i>Morganella and Providencia</i> | 0.4 | 0.8 | 0.4 | 0.0 |
| | <i>Hafnia alvei</i> | 0.8 | 0.0 | 0.0 | 0.0 |
| | NFB ^b | 0.0 | 0.4 | 1.3 | 1.1 |
| 25 | <i>Candida spp.</i> | 0.8 | 1.9 | 0.7 | 0.4 |

^a Uncommon urinary isolates are those identified as "Others" in Table 1.

30

^b NFB: non fermentative bacilli (i.e. *Stenotrophomonas* and *Acinetobacter*).

5 **Table 3.** Distribution of positive^a (bacterial count $\geq 10^7$ CFU/L) and negative (bacterial count $< 10^7$ CFU/L) urine specimens tested at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992-1994 period.

| 10 | Specimens | Number of isolates (%) | | | |
|----|-----------|------------------------|------------|-----------|------------|
| | | Nov 92 | Apr 93 | Jul 93 | Jan 94 |
| | received: | 1383(100) | 1338(100) | 1139(100) | 1345(100) |
| | positive: | 267(19.3) | 265(19.8) | 238(20.9) | 281(20.9) |
| | negative: | 1116(80.7) | 1073(80.2) | 901(79.1) | 1064(79.1) |

15

^a Based on standard diagnostic methods, the minimal number of bacterial pathogens in urine samples to indicate an urinary tract infection is normally 10^7 CFU/L.

SUBSTITUTE SHEET

Table 4. Distribution of positive and negative clinical specimens tested in the Microbiology Laboratory of the CHUL.

| 5 | Clinical specimens ^a | No. of samples tested | % of negative specimens | % of positive specimens |
|----|---------------------------------|-----------------------------|-------------------------------|-------------------------------|
| 10 | | | | |
| | Urine | 17,981 | 19.4 | 80.6 |
| | Haemoculture/marrow | 10,010 | 6.9 | 93.1 |
| | Sputum | 1,266 | 68.4 | 31.6 |
| 15 | Superficial pus | 1,136 | 72.3 | 27.7 |
| | Cerebrospinal fluid | 553 | 1.0 | 99.0 |
| | Synovial fluid-articular | 523 | 2.7 | 97.3 |
| | Bronch./Trach./Amyg./Throat | 502 | 56.6 | 43.4 |
| | Deep pus | 473 | 56.8 | 43.2 |
| 20 | Ears | 289 | 47.1 | 52.9 |
| | Pleural and pericardial fluid | 132 | 1.0 | 99.0 |
| | Peritoneal fluid | 101 | 28.6 | 71.4 |

25 ^a Specimens tested from February 1994 to January 1995.

SUBSTITUTE SHEET

Table 5. Bacterial species (66) used for testing the specificity of DNA fragment probes, oligonucleotide probes and PCR primers.

| | Bacterial species | Number of strains tested | Bacterial species | Number of strains tested |
|----|-------------------------------------|--------------------------|-------------------------------------|--------------------------|
| 10 | Gram negative: | | Gram negative: | |
| | <i>Proteus mirabilis</i> | 5 | <i>Haemophilus parainfluenzae</i> | 2 |
| 15 | <i>Klebsiella pneumoniae</i> | 5 | <i>Bordetella pertussis</i> | 2 |
| | <i>Pseudomonas aeruginosa</i> | 5 | <i>Haemophilus parahaemolyticus</i> | 2 |
| | <i>Escherichia coli</i> | 5 | <i>Haemophilus haemolyticus</i> | 2 |
| | <i>Moraxella catarrhalis</i> | 5 | <i>Haemophilus aegyptius</i> | 1 |
| | <i>Proteus vulgaris</i> | 2 | <i>Kingella indologenes</i> | 1 |
| 20 | <i>Morganella morganii</i> | 2 | <i>Moraxella atlantae</i> | 1 |
| | <i>Enterobacter cloacae</i> | 2 | <i>Neisseria caviae</i> | 1 |
| | <i>Providencia stuartii</i> | 1 | <i>Neisseria subflava</i> | 1 |
| | <i>Providencia species</i> | 1 | <i>Moraxella urethralis</i> | 1 |
| | <i>Enterobacter agglomerans</i> | 2 | <i>Shigella sonnei</i> | 1 |
| 25 | <i>Providencia rettgeri</i> | 2 | <i>Shigella flexneri</i> | 1 |
| | <i>Neisseria mucosa</i> | 1 | <i>Klebsiella oxytoca</i> | 2 |
| | <i>Providencia alcalifaciens</i> | 1 | <i>Serratia marcescens</i> | 2 |
| | <i>Providencia rustigianii</i> | 1 | <i>Salmonella typhimurium</i> | 1 |
| | <i>Burkholderia cepacia</i> | 2 | <i>Yersinia enterocolitica</i> | 1 |
| 30 | <i>Enterobacter aerogenes</i> | 2 | <i>Acinetobacter calcoaceticus</i> | 1 |
| | <i>Stenotrophomonas maltophilia</i> | 2 | <i>Acinetobacter lwoffii</i> | 1 |
| | <i>Pseudomonas fluorescens</i> | 1 | <i>Hafnia alvei</i> | 2 |
| | <i>Comamonas acidovorans</i> | 2 | <i>Citrobacter diversus</i> | 1 |
| | <i>Pseudomonas putida</i> | 2 | <i>Citrobacter freundii</i> | 1 |
| 35 | <i>Haemophilus influenzae</i> | 5 | <i>Salmonella species</i> | 1 |

...continued on next page

SUBSTITUTE SHEET

Table 5 (continued). Bacterial species (66) used for testing the specificity of DNA fragment probes, oligonucleotide probes and PCR primers.

| 10 | Bacterial species | Number of strains tested |
|-----------------------|-------------------------------------|--------------------------------|
| Gram positive: | | |
| | <i>Streptococcus pneumoniae</i> | 7 |
| 15 | <i>Streptococcus salivarius</i> | 2 |
| | <i>Streptococcus viridans</i> | 2 |
| | <i>Streptococcus pyogenes</i> | 2 |
| | <i>Staphylococcus aureus</i> | 2 |
| | <i>Staphylococcus epidermidis</i> | 2 |
| 20 | <i>Staphylococcus saprophyticus</i> | 5 |
| | <i>Micrococcus species</i> | 2 |
| | <i>Corynebacterium species</i> | 2 |
| | <i>Streptococcus groupe B</i> | 2 |
| | <i>Staphylococcus simulans</i> | 2 |
| 25 | <i>Staphylococcus ludgunensis</i> | 2 |
| | <i>Staphylococcus capitis</i> | 2 |
| | <i>Staphylococcus haemolyticus</i> | 2 |
| | <i>Staphylococcus hominis</i> | 2 |
| | <i>Enterococcus faecalis</i> | 2 |
| 30 | <i>Enterococcus faecium</i> | 1 |
| | <i>Staphylococcus warneri</i> | 1 |
| | <i>Enterococcus durans</i> | 1 |
| | <i>Streptococcus bovis</i> | 1 |
| | Diphtheroids | 1 |
| 35 | <i>Lactobacillus acidophilus</i> | 1 |

Table 6. Species-specific DNA fragment and oligonucleotide probes for hybridization.

5

| | Organisms ^a | Number of fragment probes ^b | | | Number of oligonucleotide probes | | |
|----|-----------------------------------|--|----------|-------------------------|----------------------------------|----------|-------------------------|
| | | Tested | Specific | Ubiquitous ^c | Synthesized | Specific | Ubiquitous ^c |
| 10 | | | | | | | |
| | <i>E. coli</i> ^d | - | - | - | 20 | 12 | 9 ^f |
| | <i>E. coli</i> | 14 | 2 | 2 ^e | - | - | - |
| | <i>K. pneumoniae</i> ^d | - | - | - | 15 | 1 | 1 |
| 15 | <i>K. pneumoniae</i> | 33 | 3 | 3 | 18 | 12 | 8 |
| | <i>P. mirabilis</i> ^d | - | - | - | 3 | 3 | 2 |
| | <i>P. mirabilis</i> | 14 | 3 | 3 ^e | 15 | 8 | 7 |
| | <i>P. aeruginosa</i> ^d | - | - | - | 26 | 13 | 9 |
| | <i>P. aeruginosa</i> | 6 | 2 | 2 ^e | 6 | 0 | 0 |
| 20 | <i>S. saprophyticus</i> | 7 | 4 | 4 | 20 | 9 | 7 |
| | <i>H. influenzae</i> ^d | - | - | - | 16 | 2 | 2 |
| | <i>H. influenzae</i> | 1 | 1 | 1 | 20 | 1 | 1 |
| | <i>S. pneumoniae</i> ^d | - | - | - | 6 | 1 | 1 |
| | <i>S. pneumoniae</i> | 19 | 2 | 2 | 4 | 1 | 1 |
| 25 | <i>M. catarrhalis</i> | 2 | 2 | 2 | 9 | 8 | 8 |
| | <i>S. epidermidis</i> | 62 | 1 | 1 | - | - | - |
| | <i>S. aureus</i> | 30 | 1 | 1 | - | - | - |
| | Universal probes ^d | - | - | - | 7 | - | 7 ^g |

30

^a No DNA fragment or oligonucleotide probes were tested for *E. faecalis* and *S. pyogenes*.

^b Sizes of DNA fragments range from 0.25 to 5.0 kbp.

35

^c A specific probe was considered ubiquitous when at least 80% of isolates of the target species (approximately 80 isolates) were recognized by each specific probe. When 2 or more probes are combined, 100% of the isolates are recognized.

^d These sequences were selected from data banks.

40

^e Ubiquity tested with approximately 10 isolates of the target species.

^f A majority of probes (8/9) do not discriminate *E. coli* and *Shigella* spp.

^g Ubiquity tests with a pool of the 7 probes detected all 66 bacterial species listed in Table 5.

Table 7. PCR amplification for bacterial pathogens commonly encountered in urine, sputum, blood, cerebrospinal fluid and other specimens.

| | Organism | Primer pair ^a #(SEQ ID NO) | Amplicon size (bp) | Ubiquity ^b | DNA amplification from | |
|----|-------------------------|--|-----------------------|-----------------------|------------------------|------------------------|
| | | | | | colonies ^c | specimens ^d |
| 10 | <i>E. coli</i> | 1 ^e (55+56) | 107 | 75/80 | + | + |
| | | 2 ^e (46+47) | 297 | 77/80 | + | + |
| | | 3 (42+43) | 102 | 78/80 | + | + |
| | | 4 (131+132) | 134 | 73/80 | + | + |
| 15 | | 1+3+4 | - | 80/80 | + | + |
| | <i>E. faecalis</i> | 1 ^e (38+39) | 200 | 71/80 | + | + |
| | | 2 ^e (40+41) | 121 | 79/80 | + | + |
| | | 1+2 | - | 80/80 | + | + |
| 20 | <i>K. pneumoniae</i> | 1 (67+68) | 198 | 76/80 | + | + |
| | | 2 (61+62) | 143 | 67/80 | + | + |
| | | 3 ^h (135+136) | 148 | 78/80 | + | N.T. ⁱ |
| | | 4 (137+138) | 116 | 69/80 | + | N.T. |
| | | 1+2+3 | - | 80/80 | + | N.T. |
| 25 | <i>P. mirabilis</i> | 1 (74+75) | 167 | 73/80 | + | N.T. |
| | | 2 (133+134) | 123 | 80/80 | + | N.T. |
| | <i>P. aeruginosa</i> | 1 ^e (83+84) | 139 | 79/80 | + | N.T. |
| | | 2 ^e (85+86) | 223 | 80/80 | + | N.T. |
| | <i>S. saprophyticus</i> | 1 (98+99) | 126 | 79/80 | + | + |
| | | 2 (139+140) | 190 | 80/80 | + | N.T. |
| 30 | <i>N. catarrhalis</i> | 1 (112+113) | 157 | 79/80 | + | N.T. |
| | | 2 (118+119) | 118 | 80/80 | + | N.T. |
| | | 3 (160+119) | 137 | 80/80 | + | N.T. |
| | <i>H. influenzae</i> | 1 ^e (154+155) | 217 | 80/80 | + | N.T. |
| 35 | <i>S. pneumoniae</i> | 1 ^e (156+157) | 134 | 80/80 | + | N.T. |
| | | 2 ^e (158+159) | 197 | 74/80 | + | N.T. |
| | | 3 (78+79) | 175 | 67/80 | + | N.T. |

...continued on next page

Table 7 (continued). PCR amplification for bacterial pathogens commonly encountered in urine, sputum, blood, cerebrospinal fluid and other specimens.

| Organism | Primer pair ^a #(SEQ ID NO) | Amplicon size (bp) | Ubiquity ^b | DNA amplification from | |
|---------------------------------|--|-----------------------|-----------------------|------------------------|------------------------|
| | | | | colonies ^c | specimens ^d |
| <i>S. epidermidis</i> | 1 (147+148) | 175 | 80/80 | + | N.T. |
| | 2 (145+146) | 125 | 80/80 | + | N.T. |
| <i>S. aureus</i> | 1 (152+153) | 108 | 80/80 | + | N.T. |
| | 2 (149+150) | 151 | 80/80 | + | N.T. |
| | 3 (149+151) | 176 | 80/80 | + | N.T. |
| <i>S. pyogenes</i> ^f | 1 ^e (141+142) | 213 | 80/80 | + | N.T. |
| | 2 ^e (143+144) | 157 | 24/24 | + | N.T. |
| Universal | 1 ^e (126-127) | 241 | 194/195 ^g | + | + |

20

^a All primer pairs are specific in PCR assays since no amplification was observed with DNA from 66 different species of both Gram positive and Gram negative bacteria other than the species of interest (Table 5).

25

^b The ubiquity was normally tested on 80 strains of the species of interest. All retained primer pairs amplified at least 90% of the isolates. When combinations of primers were used, an ubiquity of 100% was reached.

30

^c For all primer pairs and multiplex combinations, PCR amplifications directly performed from a bacterial colony were 100 % species-specific.

^d PCR assays performed directly from urine specimens.

^e Primer pairs derived from data bank sequences. Primer pairs with no "e" are derived from our species-specific fragments.

35

^f For *S. pyogenes*, primer pair #1 is specific for Group A Streptococci (GAS). Primer pair #2 is specific for the GAS-producing exotoxin A gene (SpeA).

40

^g Ubiquity tested on 195 isolates from 23 species representative of bacterial pathogens commonly encountered in clinical specimens.

^h Optimizations are in progress to eliminate non-specific amplification observed with some bacterial species other than the target species.

45

ⁱ N.T.: not tested.

SUBSTITUTE SHEET

Table 8. Selected antibiotic resistance genes for diagnostic purposes.

5

| | Genes | Antibiotics | Bacteria ^a | SEQ ID NO |
|----|---------------------------------------|---|--|---------------------------|
| 10 | (bla _{TEM}) TEM-1 | β-lactams | Enterobacteriaceae, Pseudomonadaceae, Haemophilus, Neisseria | 161 |
| | (bla _{ROB}) ROB-1 | β-lactams | Haemophilus, Pasteurella | 162 |
| | (bla _{SHV}) SHV-1 | β-lactams | Klebsiella and other Enterobacteriaceae | 163 |
| 15 | aacB, aacC1, aacC2, aacC3, aacA4 | Aminoglycosides | Enterobacteriaceae, Pseudomonadaceae | 164, 165, 166 167, 168 |
| | mecA | β-lactams | Staphylococci | 169 |
| | vanH, vanA, vanX | Vancomycin | Enterococci | 170 |
| 20 | sacA | Macrolides | Enterococci | 173 |
| | aacA-aphD | Aminoglycosides | Enterococci, Staphylococci | 174 |
| | vat | Macrolides | Staphylococci | 175 |
| | vga | Macrolides | Staphylococci | 176 |
| | msrA | Erythromycin | Staphylococci | 177 |
| 25 | Int and Sul conserved sequences | β-lactams, trimethoprim, aminoglycosides, anti- septic, chloramphenicol | Enterobacteriaceae, Pseudomonadaceae | 171, 172 |

30 ^a Bacteria having high incidence for the specified antibiotic resistance genes. The presence in other bacteria is not excluded.

SUBSTITUTE SHEET

**Annex I: Specific and ubiquitous oligonucleotides
probes for hybridization**

| 5 | SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
|----|--|--|--------------------------|---------------------|
| | | | SEQ ID NO | Nucleotide position |
| 10 | Bacterial species: <i>Escherichia coli</i> | | | |
| | 44 | 5'-CAC CCG CTT GCG TGG CAA GCT GCC C | 5a | 213-237 |
| | 45 | 5'-CGT TTG TGG ATT CCA GTT CCA TCC G | 5a | 489-513 |
| | 48 | 5'-TGA AGC ACT GGC CGA AAT GCT GCG T | 6a | 759-783 |
| 15 | 49 | 5'-GAT GTA CAG GAT TCG TTG AAG GCT T | 6a | 898-922 |
| | 50 | 5'-TAG CGA AGG CGT AGC AGA AAC TAA C | 7a | 1264-1288 |
| | 51 | 5'-GCA ACC CGA ACT CAA CGC CGG ATT T | 7a | 1227-1251 |
| | 52 | 5'-ATA CAC AAG GGT CGC ATC TGC GGC C | 7a | 1313-1337 |
| | 53 | 5'-TGC GTA TGC ATT GCA GAC CTT GTG GC | 7a | 111-136 |
| 20 | 54 | 5'-GCT TTC ACT GGA TAT CGC GCT TGG G | 7a | 373-397 |
| | Bacterial species: <i>Proteus mirabilis</i> | | | |
| | 70 ^b | 5'-TGG TTC ACT GAC TTT GCG ATG TTT C | 12 | 23-47 |
| | 71 | 5'-TCG AGG ATG GCA TGC ACT AGA AAA T | 12 | 53-77 |
| 25 | 72 ^b | 5'-CGC TGA TTA GGT TTC GCT AAA ATC TTA TTA | 12 | 80-109 |
| | 73 | 5'-TTG ATC CTC ATT TTA TTA ATC ACA TGA CCA | 12 | 174-203 |

^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the
sequences given in the Sequence listing

30

SUBSTITUTE SHEET

**Annex I: Specific and ubiquitous oligonucleotides
probes for hybridization**

| 5 | SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
|----|--|--|--------------------------|---------------------|
| | | | SEQ ID NO | Nucleotide position |
| 10 | <u>Bacterial species:</u> <i>Proteus mirabilis</i> | | | |
| | 76 | 5'-CCG CCT TTA GCA TTA ATT GGT GTT TAT AGT | 13 | 246-275 |
| | 77 | 5'-CCT ATT GCA GAT ACC TTA AAT GTC TTG GGC | 13 | 291-320 |
| | 80 ^b | 5'-TTG AGT GAT GAT TTC ACT GAC TCC C | 14 | 18-42 |
| | 81 | 5'-GTC AGA CAG TGA TGC TGA CGA CAC A | 15 ^a | 1185-1209 |
| 15 | 82 | 5'-TGG TTG TCA TGC TGT TTG TGT GAA AAT | 15 ^a | 1224-1250 |
| | <u>Bacterial species:</u> <i>Klebsiella pneumoniae</i> | | | |
| | 57 | 5'-GTG GTG TCG TTC AGC GCT TTC AC | 8 | 45-67 |
| | 58 | 5'-GCG ATA TTC ACA CCC TAC GCA GCC A | 9 | 161-185 |
| 20 | 59 ^b | 5'-GTC GAA AAT GCC GGA AGA GGT ATA CG | 9 | 203-228 |
| | 60 ^b | 5'-ACT GAG CTG CAG ACC GGT AAA ACT CA | 9 | 233-258 |
| | 63 ^b | 5'-CGT GAT GGA TAT TCT TAA CGA AGG GC | 10 | 250-275 |
| | 64 ^b | 5'-ACC AAA CTG TTG AGC CGC CTG GA | 10 | 201-223 |
| | 65 | 5'-GTG ATC GCC CCT CAT CTG CTA CT | 10 | 77-99 |
| 25 | 66 | 5'-CGC CCT TCG TTA AGA ATA TCC ATC AC | 10 | 249-274 |
| | 69 | 5'-CAG GAA GAT GCT GCA CCG GTT GTT G | 11 ^a | 296-320 |

^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the

30 sequences given in the Sequence listing

SUBSTITUTE SHEET

**Annex I: Specific and ubiquitous oligonucleotides
probes for hybridization**

| 5 | SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
|----|---|--------------------------------------|--------------------------|---------------------|
| | | | SEQ ID NO | Nucleotide position |
| 10 | Bacterial species: <i>Pseudomonas aeruginosa</i> | | | |
| | 87 | 5'-AAT GCG GCT GTA CCT CGG CGC TGG T | 18 ^a | 2985-3009 |
| | 88 | 5'-GGC GGA GGG CCA GTT GCA CCT GCC A | 18 ^a | 2929-2953 |
| | 89 | 5'-AGC CCT GCT CCT CGG CAG CCT CTG C | 18 ^a | 2821-2845 |
| | 90 | 5'-TGG CTT TTG CAA CCG CGT TCA GGT T | 18 ^a | 1079-1103 |
| 15 | 91 | 5'-GCG CCC GCG AGG GCA TGC TTC GAT G | 19 ^a | 705-729 |
| | 92 | 5'-ACC TGG GCG CCA ACT ACA AGT TCT A | 19 ^a | 668-692 |
| | 93 | 5'-GGC TAC GCT GCC GGG CTG CAG GCC G | 19 ^a | 505-529 |
| | 94 | 5'-CCG ATC TAC ACC ATC GAG ATG GGC G | 20 ^a | 1211-1235 |
| | 95 | 5'-GAG CGC GGC TAT GTG TTC GTC GGC T | 20 ^a | 2111-2135 |
| 20 | Bacterial species: <i>Streptococcus pneumoniae</i> | | | |
| | 120 | 5'-TCT GTG CTA GAG ACT GCC CCA TTT C | 30 | 423-447 |
| | 121 | 5'-CGA TGT CTT GAT TGA GCA GGG TTA T | 31 ^a | 1198-1222 |
| 25 | ^a Sequences from data banks | | | |
| | ^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing | | | |

SUBSTITUTE SHEET

**Annex I: Specific and ubiquitous oligonucleotides
probes for hybridization**

| 5 | SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
|----|---|--|--------------------------|---------------------|
| | | | SEQ ID NO | Nucleotide position |
| 10 | Bacterial species: <i>Staphylococcus saprophyticus</i> | | | |
| | 96 | 5'-CGT TTT TAC CCT TAC CTT TTC GTA CTA CC | 21 | 45-73 |
| | 97 ^b | 5'-TCA GGC AGA GGT AGT ACG AAA AGG TAA GGG | 21 | 53-82 |
| | 100 | 5'-CAC CAA GTT TGA CAC GTG AAG ATT CAT | 22 | 89-115 |
| | 101 ^b | 5'-ATG AGT GAA GCG GAG TCA GAT TAT GTG CAG | 23 | 105-134 |
| 15 | 102 | 5'-CGC TCA TTA CGT ACA GTG ACA ATC G | 24 | 20-44 |
| | 103 | 5'-CTG GTT AGC TTG ACT CTT AAC AAT CTT GTC | 24 | 61-90 |
| | 104 ^b | 5'-GAC GCG ATT GTC ACT GTA CGT AAT GAG CGA | 24 | 19-48 |
| | Bacterial species: <i>Moraxella catarrhalis</i> | | | |
| 20 | 108 | 5'-GCC CCA AAA CAA TGA AAC ATA TGG T | 28 | 81-105 |
| | 109 | 5'-CTG CAG ATT TTG GAA TCA TAT CGC C | 28 | 126-150 |
| | 110 | 5'-TGG TTT GAC CAG TAT TTA ACG CCA T | 28 | 165-189 |
| | 111 | 5'-CAA CGG CAC CTG ATG TAC CTT GTA C | 28 | 232-256 |
| | 114 | 5'-TTA CAA CCT GCA CCA CAA GTC ATC A | 29 | 97-121 |
| 25 | 115 | 5'-GTA CAA ACA AGC CGT CAG CGA CTT A | 29 | 139-163 |
| | 116 | 5'-CAA TCT GCG TGT GTG CGT TCA CT | 29 | 178-200 |
| | 117 | 5'-GCT ACT TTG TCA GCT TTA GCC ATT CA | 29 | 287-312 |

^a Sequences from data banks

30 ^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

SUBSTITUTE SHEET

**Annex I: Specific and ubiquitous oligonucleotides
probes for hybridization**

| | | | | |
|----|---|---|--------------------------|---------------------|
| 5 | SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
| | | | SEQ ID NO | Nucleotide position |
| 10 | Bacterial species: <i>Haemophilus influenzae</i> | | | |
| | 105 ^b | 5'-GCG TCA GAA AAA GTA GGC GAA ATG AAA G | 25 | 138-165 |
| | 106 ^b | 5'-AGC GGC TCT ATC TTG TAA TGA CAC A | 26 ^a | 770-794 |
| | 107 ^b | 5'-GAA ACG TGA ACT CCC CTC TAT ATA A | 27 ^a | 5184-5208 |
| 15 | Universal probes^c | | | |
| | 122 ^b | 5'-ATC CCA CCT TAG GCG GCT GGC TCC A | - | - |
| | 123 | 5'-ACG TCA AGT CAT CAT GGC CCT TAC GAG TAG G | - | - |
| | 124 ^b | 5'-GTG TGA CGG GCG GTG TGT ACA AGG C | - | - |
| | 125 ^b | 5'-GAG TTG CAG ACT CCA ATC CGG ACT ACG A | - | - |
| 20 | 128 ^b | 5'-CCC TAT ACA TCA CCT TGC GGT TTA GCA GAG AG | - | - |
| | 129 | 5'-GGG GGG ACC ATC CTC CAA GGC TAA ATA C | - | - |
| | 130 ^b | 5'-CGT CCA CTT TCG TGT TTG CAG AGT GCT GTG TT | - | - |

^a Sequences from data banks

25 ^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

^c Universal probes were derived from 16S or 23S ribosomal RNA gene sequences not included in the Sequence listing

**Annex II: Specific and ubiquitous primers for DNA
amplification**

| 5 | SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
|----|--|-------------------------------|--------------------------|---------------------|
| | | | SEQ ID NO | Nucleotide position |
| 10 | <u>Bacterial species:</u> <i>Escherichia coli</i> | | | |
| | 42 | 5'-GCT TTC CAG CGT CAT ATT G | 4 | 177-195 |
| | 43 ^b | 5'-GAT CTC GAC AAA ATG GTG A | 4 | 260-278 |
| | 46 | 5'-TCA CCC GCT TGC GTG GC | 5 ^a | 212-228 |
| | 47 ^b | 5'-GGA ACT GGA ATC CAC AAA C | 5 ^a | 490-508 |
| 15 | 55 | 5'-GCA ACC CGA ACT CAA CGC C | 7 ^a | 1227-1245 |
| | 56 ^b | 5'-GCA GAT GCG ACC CTT GTG T | 7 ^a | 1315-1333 |
| | 131 | 5'-CAG GAG TAC GGT GAT TTT TA | 3 | 60-79 |
| | 132 ^b | 5'-ATT TCT GGT TTG GTC ATA CA | 3 | 174-193 |
| 20 | <u>Bacterial species:</u> <i>Enterococcus faecalis</i> | | | |
| | 38 | 5'-GCA ATA CAG GGA AAA ATG TC | 1 ^a | 69-88 |
| | 39 ^b | 5'-CTT CAT CAA ACA ATT AAC TC | 1 ^a | 249-268 |
| | 40 | 5'-GAA CAG AAG AAG CCA AAA AA | 2 ^a | 569-588 |
| | 41 ^b | 5'-GCA ATC CCA AAT AAT ACG GT | 2 ^a | 670-689 |
| 25 | | | | |

^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

SUBSTITUTE SHEET

**Annex II: Specific and ubiquitous primers for DNA
amplification**

| 5 | SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
|----|--|-------------------------------|--------------------------|---------------------|
| | | | SEQ ID NO | Nucleotide position |
| 10 | Bacterial species: <i>Klebsiella pneumoniae</i> | | | |
| | 61 | 5'-GAC AGT CAG TTC GTC AGC C | 9 | 37-55 |
| | 62 ^b | 5'-CGT AGG GTG TGA ATA TCG C | 9 | 161-179 |
| | 67 | 5'-TCG CCC CTC ATC TGC TAC T | 10 | 81-99 |
| 15 | 68 ^b | 5'-GAT CGT GAT GGA TAT TCT T | 10 | 260-278 |
| | 135 | 5'-GCA GCG TGG TGT CGT TCA | 8 | 40-57 |
| | 136 ^b | 5'-AGC TGG CAA CGG CTG GTC | 8 | 170-187 |
| | 137 | 5'-ATT CAC ACC CTA CGC AGC CA | 9 | 166-185 |
| | 138 ^b | 5'-ATC CGG CAG CAT CTC TTT GT | 9 | 262-281 |
| 20 | Bacterial species: <i>Proteus mirabilis</i> | | | |
| | 74 | 5'-GAA ACA TCG CAA AGT CAG T | 12 | 23-41 |
| | 75 ^b | 5'-ATA AAA TGA GGA TCA AGT TC | 12 | 170-189 |
| | 133 | 5'-CGG GAG TCA GTG AAA TCA TC | 14 | 17-36 |
| 25 | 134 ^b | 5'-CTA AAA TCG CCA CAC CTC TT | 14 | 120-139 |

^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

SUBSTITUTE SHEET

**Annex II: Specific and ubiquitous primers for DNA
amplification**

| 5 | SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
|----|---|--|--------------------------|---------------------|
| | | | SEQ ID NO | Nucleotide position |
| 10 | Bacterial species: <i>Staphylococcus saprophyticus</i> | | | |
| | 98 | 5'-CGT TTT TAC CCT TAC CTT TTC GTA CT | 21 | 45-70 |
| | 99 ^b | 5'-ATC GAT CAT CAC ATT CCA TTT GTT TTT A | 21 | 143-170 |
| | 139 | 5'-CTG GTT AGC TTG ACT CTT AAC AAT C | 24 | 61-85 |
| | 140 ^b | 5'-TCT TAA CGA TAG AAT GGA GCA ACT G | 24 | 226-250 |
| 15 | Bacterial species: <i>Pseudomonas aeruginosa</i> | | | |
| | 83 | 5'-CGA GCG GGT GGT GTT CAT C | 16 ^a | 554-572 |
| | 84 ^b | 5'-CAA GTC GTC GTC GGA GGG A | 16 ^a | 674-692 |
| | 85 | 5'-TCG CTG TTC ATC AAG ACC C | 17 ^a | 1423-1441 |
| 20 | 86 ^b | 5'-CCG AGA ACC AGA CTT CAT C | 17 ^a | 1627-1645 |
| | Bacterial species: <i>Moraxella catarrhalis</i> | | | |
| | 112 | 5'-GGC ACC TGA TGT ACC TTG | 28 | 235-252 |
| | 113 ^b | 5'-AAC AGC TCA CAC GCA TT | 28 | 375-391 |
| 25 | 118 | 5'-TGT TTT GAG CTT TTT ATT TTT TGA | 29 | 41-64 |
| | 119 ^b | 5'-CGC TGA CGG CTT GTT TGT ACC A | 29 | 137-158 |
| | 160 | 5'-GCT CAA ATC AGG GTC AGC | 29 | 22-39 |
| | 119 ^b | 5'-CGC TGA CGG CTT GTT TGT ACC A | 29 | 137-158 |

30 ^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

SUBSTITUTE SHEET

**Annex II: Specific and ubiquitous primers for DNA
amplification**

| 5 | SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
|----|---|--|--------------------------|---------------------|
| | | | SEQ ID NO | Nucleotide position |
| 10 | Bacterial species: <i>Staphylococcus epidermidis</i> | | | |
| | 145 | 5'-ATC AAA AAG TTG GCG AAC CTT TTC A | 36 | 21-45 |
| | 146 ^b | 5'-CAA AAG AGC GTG GAG AAA AGT ATC A | 36 | 121-145 |
| | 147 | 5'-TCT CTT TTA ATT TCA TCT TCA ATT CCA TAG | 36 | 448-477 |
| | 148 ^b | 5'-AAA CAC AAT TAC AGT CTG GTT ATC CAT ATC | 36 | 593-622 |
| 15 | Bacterial species: <i>Staphylococcus aureus</i> | | | |
| | 149 ^b | 5'-CTT CAT TTT ACG GTG ACT TCT TAG AAG ATT | 37 | 409-438 |
| | 150 | 5'-TCA ACT GTA GCT TCT TTA TCC ATA CGT TGA | 37 | 288-317 |
| | 149 ^b | 5'-CTT CAT TTT ACG GTG ACT TCT TAG AAG ATT | 37 | 409-438 |
| 20 | 151 | 5'-ATA TTT TAG CTT TTC AGT TTC TAT ATC AAC | 37 | 263-292 |
| | 152 | 5'-AAT CTT TGT CGG TAC ACG ATA TTC TTC ACG | 37 | 5-34 |
| | 153 ^b | 5'-CGT AAT GAG ATT TCA GTA GAT AAT ACA ACA | 37 | 83-112 |

25 ^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

SUBSTITUTE SHEET

**Annex II: Specific and ubiquitous primers for DNA
amplification**

5

| SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
|---|---------------------------------------|--------------------------|---------------------|
| | | SEQ ID NO | Nucleotide position |
| Bacterial species: <i>Haemophilus influenzae</i> | | | |
| 154 | 5'-TTT AAC GAT CCT TTT ACT CCT TTT G | 27 ^a | 5074-5098 |
| 155 ^b | 5'-ACT GCT GTT GTA AAG AGG TTA AAA T | 27 ^a | 5266-5290 |
| Bacterial species: <i>Streptococcus pneumoniae</i> | | | |
| 78 | 5'-AGT AAA ATG AAA TAA GAA CAG GAC AG | 34 | 164-189 |
| 79 ^b | 5'-AAA ACA GGA TAG GAG AAC GGG AAA A | 34 | 314-338 |
| 156 | 5'-ATT TGG TGA CGG GTG ACT TT | 31 ^a | 1401-1420 |
| 157 ^b | 5'-GCT GAG GAT TTG TTC TTC TT | 31 ^a | 1515-1534 |
| 158 | 5'-GAG CGG TTT CTA TGA TTG TA | 35 ^a | 1342-1361 |
| 159 ^b | 5'-ATC TTT CCT TTC TTG TTC TT | 35 ^a | 1519-1538 |
| Bacterial species: <i>Streptococcus pyogenes</i> | | | |
| 141 | 5'-TGA AAA TTC TTG TAA CAG GC | 32 ^a | 286-305 |
| 142 ^b | 5'-GGC CAC CAG CTT GCC CAA TA | 32 ^a | 479-498 |
| 143 | 5'-ATA TTT TCT TTA TGA GGG TG | 33 ^a | 966-985 |
| 144 ^b | 5'-ATC CTT AAA TAA AGT TGC CA | 33 ^a | 1103-1122 |

^a Sequences from data banks

30 ^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

SUBSTITUTE SHEET

Annex II: Specific and ubiquitous primers for DNA amplification

| | | | | |
|----|--------------------------------|-------------------------------|--------------------------|---------------------|
| 5 | SEQ ID NO | Nucleotide sequence | Originating DNA fragment | |
| | | | SEQ ID NO | Nucleotide position |
| | Universal primers ^c | | | |
| 10 | 126 | 5'-GGA GGA AGG TGG GGA TGA CG | - | - |
| | 127 ^b | 5'-ATG GTG TGA CGG GCG GTG TG | - | - |

^a Sequences from data banks

15 ^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

^c Universal primers were derived from the 16S ribosomal RNA gene sequence not included in the Sequence listing

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

Reverse strand of SEQ ID NO: 122 TGGAGCC AGCCGCCTAA GGTGGGAT

| | | | |
|--------------------------|------------|------------|-----------------------------------|
| | | | 1510 |
| | 1461 | | |
| Streptococcus salivarius | TGAGGTAACC | TTTTGGAGCC | AGCCGCCTAA GGTGGGATAG ATGANNNGGG |
| Proteus vulgaris | TAGCTTAACC | TTCGGGAGGG | CGCTTACCAC TTGTGTGATTC ATGACTGGGG |
| Pseudomonas aeruginosa | TAGTCTAACC | GCAAGGGGGG | CGGTACCAC GGAAGTGATTC ATGACTGGGG |
| Neisseria gonorrhoeae | TAGGGTAACC | GCAAGGAGTC | CGCTTACCAC GGTATGCTTC ATGACTGGGG |
| Streptococcus lactis | TTGCCTAACC | GCAAGGAGGG | CGCTTCCTAA GGTAAAGACCG ATGACNNGGG |

5

10

15

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

5

| | SEQ ID NO: | 123 | | 1300 |
|----|-------------------------|-------------|-------------------------|-----------------------------------|
| | | ACGTCAAAGTC | ATCATGGC CCTTACGAGT AAG | |
| 10 | Haemophilus influenzae | GGTNGGGGATG | ACGTCAAAGTC | ..ATCATGGC CCTTACGAGT AGGGCTACAC |
| | Neisseria gonorrhoeae | GGTGGGGATG | ACGTCAAAGTC | ..CTCATGGC CCTTATGACC AGGGCTTCAC |
| | Pseudomonas cepacia | GGTNGGGGATG | ACGTCAAAGTC | ..CTCATGGC CCTTATGGGT AGGGCTTCAC |
| | Serratia marcescens | GGTGGGGATG | ACGTCAAAGTC | ..ATCATGGC CCTTACGAGT AGGGCTACAC |
| | Escherichia coli | GGTGGGGATG | ACGTCAAAGTC | ..ATCATGGC CCTTACGACC AGGGCTACAC |
| 15 | Proteus vulgaris | GGTGGGGATG | ACGTTAAAGTC | GTATCATGGC CCTTACGAGT AGGGCTACAC |
| | Pseudomonas aeruginosa | GGTGGGGATG | ACGTCAAAGTC | ..ATCATGGC CCTTACGGCN AGGGCTACAC |
| | Clostridium perfringens | GGTGGGGATG | ACGTNNAATC | ..ATCATGGC CNTTATGTGT AGGGCTACAC |
| | Mycoplasma hominis | GGTGGGGATG | ACGTCAAATC | ..ATCATGGC TCTTACGAGT GGGGCCACAC |
| | H. licobacter pylori | GGTGGGGACG | ACGTCAAAGTC | ..ATCATGGC CCTTACGCCCT AGGGCTACAC |
| 20 | Mycoplasma pneumoniae | GGAAGGGATG | ACGTCAAATC | ..ATCATGGC CCTTATGTCT AGGGCTGCAA |

51

SUBSTITUTE SHEET

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

5

| Reverse of the probe SEQ ID NO: 124 | | GCCTTGTACA CACCGCCCGT CACAC |
|-------------------------------------|--------------------------------|-----------------------------|
| 10 | <i>Escherichia coli</i> | 1451 |
| | <i>Neisseria gonorrhoeae</i> | 1490 |
| | <i>Pseudomonas cepacia</i> | |
| | <i>Serratia marcescens</i> | |
| | <i>Proteus vulgaris</i> | |
| 15 | <i>Haemophilus influenzae</i> | |
| | <i>Pseudomonas aeruginosa</i> | |
| | <i>Clostridium perfringens</i> | |
| | <i>Mycoplasma hominis</i> | |
| | <i>Helicobacter pylori</i> | |
| 20 | <i>Mycoplasma pneumoniae</i> | |

Ann x III. Selection of universal probes by alignment of the
sequences of bacterial 16S and 23S ribosomal RNA genes.

5

| Reverse strand of SEQ ID NO 125: | | | |
|----------------------------------|-----------------------|------------------------|--|
| | TCG TAGTCCGGAT | TGGAGTCTGC AACTC | |
| 10 | 1361 | 1400 | |
| <i>Esch richia coli</i> | AAGTGGTCC TAGTCCGGAT | TGGAGTCTGC AACTCGACTC | |
| <i>N isseria gonorrhoeae</i> | AAACCGATCC TAGTCCGGAT | TGCACCTCTGC AACTCGAGTG | |
| <i>Pseudomonas cepacia</i> | AAACCGATCC TAGTCCGGAT | TGCACCTCTGC AACTCGAGTG | |
| <i>Serratia marcescens</i> | AAGTATGTCG TAGTCCGGAT | TGGAGTCTGC AACTCGACTC | |
| <i>Prot us vulgaris</i> | AAGTCTGTCG TAGTCCGGAT | TGGAGTCTGC AACTCGACTC | |
| <i>Haemophilus influenzae</i> | AAGTACGTCT AAGTCCGGAT | TGGAGTCTGC AACTCGACTC | |
| <i>Pseudomonas aeruginosa</i> | AAACCGATCC TAGTCCGGAT | CGCAGTCTGC AACTCGACTG | |
| <i>Clostridium perfringens</i> | AAACCGATCT CAGTTCGGAT | TGTAGGCTGA AACTCGCCTA | |
| <i>Mycoplasma hominis</i> | AAGCCGATCT CAGTTCGGAT | TGGAGTCTGC AATTGACTC | |
| <i>Helicobacter pylori</i> | ACACC..TCT CAGTTCGGAT | TGTAGGCTGC AACTCGCCTG | |
| 20 <i>Mycoplasma pneumoniae</i> | AAGTTGGTCT CAGTTCGGAT | TGAGGGCTGC AATTGTCCT | |

SUBSTITUTE SHEET

Ann x III. Selection of universal probes by alignment of the
sequences of bacterial 16S and 23S ribosomal RNA genes.

5

R v rse strand of SEQ ID NO: 128 CT CTCTGCTAAA CCGCAAGGTG ATGTATAGGG

| | | |
|----|-----------------------------|---|
| | 1991 | 2040 |
| 10 | Lactobacillus lactis | AAACACAGCT CTCTGCTAAA CCGCAAGGTG ATGTATAGGG GGTGACGCCT |
| | Escherichia coli | AAACACAGCA CTGTGCAAAAC ACGAAAGTGG ACGTATACGG TGTGACGCCT |
| | Pseudomonas aeruginosa | AAACACAGCA CTCTGCAAAAC ACGAAAGTGG ACGTATAGGG TGTGACGCCT |
| | Pseudomonas cepacia | AAACACAGCA CTCTGCAAAAC ACGAAAGTGG ACGTATAGGG TGTGACGCCT |
| | Bacillus stearothermophilus | AAACACAGGT CTCTGCGAAG TCGTAAAGCG ACGTATAGGG GCTGACACCT |
| 15 | Micrococcus luteus | AAACACAGGT CCATGCGAAG TCGTAAAGCG ATGTATATGG ACTGACTCCT |

54

SEQ ID NO: 129

| | | |
|----|-------------------------|---|
| | 481 | 530 |
| 20 | Escherichia coli | TGTCTGAATA TGGGGGGACC ATCCTCCAA GCTAAATACT CCTGACTGAC |
| | Pseudomonas aeruginosa. | TGTCTGAACA TGGGGGGACC ATCCTCCAA GCTAAATACT ACTGACTGAC |
| | Pseudomonas cepacia | TGTCTGAAGA TGGGGGGACC ATCCTCCAA GCTAAATACT CGTGATCGAC |
| | Lactobacillus lactis | AGTTTGAATC CGGGAGGACC ATCTCCCAA CCTAAATACT CCTTAGTGAC |
| | Micrococcus luteus | CGTGTGAATC TGCCAGGACC ACCTGGTAA GCTGAATACT ACCTGTTGAC |

SUBSTITUTE SHEET

Annex III. Selection of universal probes by alignment of the
sequences of bacterial 16S and 23S ribosomal RNA genes.

5

| Rev rse strand of SEQ ID NO: 130 | | AACACACAGCA CTCTGCAAAAC ACGAAAAGTGG ACG | |
|----------------------------------|------------|---|------------|
| | | | |
| | 1981 | | 2030 |
| 10 Pseudomonas aeruginosa | TGTTTATTAA | AAACACACAGCA CTCTGCAAAAC ACGAAAAGTGG | ACGTATAGGG |
| Escherichia coli | TGTTTATTAA | AAACACACAGCA CTCTGCAAAAC ACGAAAAGTGG | ACGTATACGG |
| Pseudomonas cepacia | TGTTTAAATA | AAACACACAGCA CTCTGCAAAAC ACGAAAAGTGG | ACGTATAGGG |
| Bacillus stearothermophilus | TGTTTATCAA | AAACACACAGGT CTCTGCGAAG TCGTAAAGGCG | ACGTATAGGG |
| Lactobacillus lactis | TGTTTATCAA | AAACACACAGCT CTCTGCTAAA CCGCAAGGTG | ATGTATAGGG |
| 15 Micrococcus luteus | TGTTTATCAA | AAACACACAGGT CCATGCGAAG TCGTAAAGACG | ATGTATATGG |

SUBSTITUTE SHEET

**Annex IV. Selection of the universal PCR primers by alignment of the
bacterial 16S ribosomal RNA gene**

SEQ ID NO: 126 GGAGGAA GGTGGGATG ACG

Reverse strand of SEQ ID NO: 127

CA CACCGCCCGT CACACCAT

10

1270.....1461

1241

1490

Escherichia coli

ACTGGAGGAA GGTGGGATG ACCTCAAGTC.....GCCTTGATCA

CACCGCCCGT CACACCATGG

Neisseria gonorrhoeae

GCCGGAGGAA GGTGGGATG ACCTCAAGTC.....NNCTTGATCA

CACCGCCCGT CACACCATGG

Psudomonas cepacia

ACCGGAGGAA GGTGGGATG ACCTCAAGTC.....GTCTTGATCA

CACCGCCCGT CACACCATGG

Serratia marcescens

ACTGGAGGAA GGTGGGATG ACCTCAAGTC.....GCCTTGATCA

CACCGCCCGT CACACCATGG

Proteus vulgaris

ACCGGAGGAA GGTGGGATG ACCTTAAGTC.....GCCTTGATCA

CACCGCCCGT CACACCATGG

Haemophilus influenzae

ACTGGAGGAA GGTGGGATG ACCTCAAGTC.....GCNTTGATCA

CACCGCCCGT CACACCATGG

Legionella pneumophila

ACCGGAGGAA GGTGGGATG ACCTCAAGTC.....GCCTTGATCA

CACCGCCCGT CACACCATGG

Pseudomonas aeruginosa

ACCGGAGGAA GGTGGGATG ACCTCAAGTC.....GCCTTGATCA

CACCGCCCGT CACACCATGG

Clostridium perfringens

CCAGGAGGAA GGTGGGATG ACCTNNAATC.....GTCTTGATCA

CACCGCCCGT CACACCATGG

20

Mycoplasma hominis

CTGGGAGGAA GGTGGGATG ACCTCAATC.....GTCTTGATCA

CACCGCCCGT CACACCATGG

Helicobacter pylori

GGAGGAGGAA GGTGGGATG ACCTCAAGTC.....GTCTTGATCA

CACCGCCCGT CACACCATGG

Mycoplasma pneumoniae

ATTGGAGGAA GGTGGGATG ACCTCAATC.....GTCTTGATCA

CACCGCCCGT CACACCATGG

SUBSTITUTE SHEET

57

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: BERGERON, Michel G.
OUELLETTE, Marc
ROY, Paul H.
- (ii) TITLE OF THE INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON
BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM
CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN MICROBIOLOGY
LABORATORIES
- (iii) NUMBER OF SEQUENCES: 177
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE:
 - (B) STREET:
 - (C) CITY:
 - (D) STATE:
 - (E) COUNTRY:
 - (F) ZIP:
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: FLOPPY DISK, 800K
 - (B) COMPUTER: Macintosh IIci
 - (C) OPERATING: System 7.0
 - (D) SOFTWARE: Word 5.1a
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: JEAN C. BAKER
 - (B) REGISTRATION NUMBER:
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE:
 - (B) TELEFAX:

SUBSTITUTE SHEET

58

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1817 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

| | | | | | |
|------------|------------|------------|-------------|------------|------|
| ACAGTAAAAA | AGTTGTTAAC | GAATGAATTT | GTTAACAAC | TTTTTGCTAT | 50 |
| GGTATTGAGT | TATGAGGGGC | AATACAGGGA | AAAATGTCGG | CTGATTAAGG | 100 |
| AATTTAGATA | GTGCCGGTTA | GTAGTTGTCT | ATAATGAAAA | TAGCAACAAA | 150 |
| TATTTACGCA | GGGAAAGGGG | CGGTCGTTTA | ACGGGAAAAA | TTAGGGAGGA | 200 |
| TAAAGCAATA | CTTTTGTTGG | GAAAAGAAAT | AAAAGGAAAC | TGGGGAAGGA | 250 |
| GTTAATTGTT | TGATGAAGGG | AAATAAAATT | TTATACATTT | TAGGTACAGG | 300 |
| CATCTTTGTT | GGAAGTTCAT | GTCTATTTTC | TTCACTTTTT | GTAGCCGCAG | 350 |
| AAGAACAAGT | TTATTCAGAA | AGTGAAGTTT | CAACAGTTTT | ATCGAAGTTG | 400 |
| GAAAAGGAGG | CAATTTCTGA | GGCAGCTGCT | GAACAATATA | CGGTTGTAGA | 450 |
| TCGAAAAGAA | GACGCGTGCG | GGATGAAGCA | TCTTAAGTTA | GAAAAGCAAA | 500 |
| CGGAAGGCGT | TACTGTTGAT | TCAGATAATG | TGATTATTCA | TTTAGATAAA | 550 |
| AACGGTGCAG | TAACAAGTGT | TACAGGAAAT | CCAGTTGATC | AAGTTGTGAA | 600 |
| AATTCAATCG | GTTGATGCAA | TCGGTGAAGA | AGGAGTTAAA | AAAATTGTTG | 650 |
| CTTCTGATAA | TCCAGAAACT | AAAGATCTTG | TCTTTTTTAGC | TATTGACAAA | 700 |
| CGTGTAATAA | ATGAAGGGCA | ATTATTTTAT | AAAGTCAGAG | TAACCTCTTC | 750 |
| ACCAACTGGT | GACCCCGTAT | CATTGGTTTA | TAAAGTGAAC | GCTACAGATG | 800 |
| GAACAATTAT | GGAAAAACAA | GATTTAACGG | AACATGTCGG | TAGTGAAGTA | 850 |
| ACGTTAAAAA | ACTCTTTTCA | AGTAACGTTT | AATGTACCAG | TTGAAAAAAG | 900 |
| CAATACGGGA | ATTGCTTTAC | ACGGAACGGA | TAACACAGGG | GTTTACCATG | 950 |
| CAGTAGTTGA | TGGCAAAAAT | AATTATTCTA | TTATTCAAGC | GCCATCACTA | 1000 |
| GCGACATTAA | ATCAGAATGC | TATTGACGCC | TATACGCATG | GAAAATTTGT | 1050 |
| GAAAACATAT | TATGAAGATC | ATTTCCAACG | ACACAGTATT | GATGATCGAG | 1100 |
| GGATGCCCAT | CTTGTCAGTT | GTTGATGAAC | AACATCCAGA | TGCTTATGAC | 1150 |
| AATGCTTTTT | GGGATGGAAA | AGCAATGCGT | TATGGTGAAA | CAAGTACACC | 1200 |
| AACAGGAAAA | ACGTATGCTT | CCTCTTTAGA | TGTAGTTGGT | CATGAAATGA | 1250 |
| CACATGGTGT | GACGGAACAT | ACTGCCGGTT | TAGAATATTT | AGGACAATCA | 1300 |
| GGTGCCTTGA | ATGAATCTTA | TTCTGATTTG | ATGGGTTATA | TTATTTCCGG | 1350 |

SUBSTITUTE SHEET

59

| | | | | | |
|-------------|-------------|------------|------------|------------|------|
| TGCATCTAAT | CCAGAAATTG | GTGCGGATAC | TCAGAGTGTT | GACCGAAAAA | 1400 |
| CAGGTATTCTG | AAATTTACAA | ACGCCAAGTA | AACACGGACA | ACCAGAAACC | 1450 |
| ATGGCTCAAT | ACGACGATCG | AGCACGGTAT | AAAGGAACGC | CTTATTATGA | 1500 |
| TCAAGGCGGT | GTTCAATTATA | ACAGTGGAAT | TATTAATCGG | ATTGGTTACA | 1550 |
| CCATTATCCA | GAACCTTAGGC | ATTGAAAAAG | CACAGACTAT | TTTCTACAGC | 1600 |
| TCGTTAGTAA | ATTACTTAAC | ACCTAAAGCA | CAATTCAGTG | ATGCTCGTGC | 1650 |
| TGCGATGCTT | GCTGCTGCAA | AAGTTCAATA | TGGCGATGAA | GCAGCTTCAG | 1700 |
| TGGTGTGACG | AGCCTTTAAC | TCTGCTGGAA | TCGGAGCTAA | AGAAGACATT | 1750 |
| CAGGTAAACC | AACCAAGTGA | ATCTGTTCTG | GTCAATGAAT | GAAAAAAATT | 1800 |
| CCCCAATTAA | ATAAAAAA | | | | 1817 |

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2275 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

| | | | | | |
|------------|-------------|------------|-------------|------------|-----|
| GGTACCAAAG | AAAAAAACGA | ACGCCACAAC | CAACAGCCTC | TAAAGCAACA | 50 |
| CCTGCTTCTG | AAATTGAGGG | AGATTTAGCA | AATGTCAATG | AGATTCTTTT | 100 |
| GGTTCACGAT | GATCGTGTCTG | GGTCAGCAAC | GATGGGAATG | AAAGTCTTAG | 150 |
| AAGAAATTTT | AGATAAAGAG | AAAATTTCAA | TGCCGATTCTG | AAAAATTAAT | 200 |
| ATTAATGAAT | TAACCTCAACA | AACACAGGCT | TTAATTGTCA | CAAAAGCTGA | 250 |
| ACTAACGGAA | CAAGCACGTA | AAAAGCACC | GAAAGCGACA | CACTTATCAG | 300 |
| TAAAAAGTTA | TGGTTAATCC | CCAAAAATAT | GAAACAGTGG | GTTTCGCTCT | 350 |
| TAAAAGAAAG | TGCCTAGAGA | GGAAGAAAAC | AATGGAAAAT | CTTACGAATA | 400 |
| TTTCAATTGA | ATTAAATCAA | CAGTTTAATA | CAAAAGAAGA | AGCTATTCGC | 450 |
| TTTTCGGGCC | AGAAACTAGT | CGAGGCAGGC | TGTGTTGAGC | CCGCTTATAT | 500 |
| CGAAGCAATG | ATTGAAAGAG | ACCAATTGCT | ATCTGCCCCT | ATGGGGAATT | 550 |
| TTATTGCCAT | TCCTCATGGA | ACAGAAGAAG | CCAAAAAATT | AGTGAAAAAA | 600 |
| TCAGGAATCT | GTGTAGTGCA | AGTCCCAGAG | GGCGTTAATT | TTGGCACCGA | 650 |
| AGAAGATGAA | AAAATTGCTA | CCGTATTATT | TGGGATTGCC | GGAGTCGGTG | 700 |
| AAGAACATTT | GCAATTAGTC | CAACAAATTG | CACTTTATTG | TAGTGATATG | 750 |
| GATAACGTGG | TGCAACTTGC | CGATGCATTA | AGTAAAGAAG | AAATAACAGA | 800 |

SUBSTITUTE SHEET

60

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| GATCCGCCAT | GGGTTGTTTT | CCGATTGAGG | ATTTTATAGA | TGGTTTCTGG | 50 |
| CGACCTGCAC | AGGAGTACGG | TGATTTTTAA | TTATTGCAAT | TGCACAAGAG | 100 |
| TCAGTTCTCC | CCCAAAGACA | GCACCGGTAT | CAATATAATG | CAGGTTGCCA | 150 |
| ATATCCACGC | GATGGCGCAA | AGGTGTATGA | CCAAACCAGA | AATGATCGGC | 200 |
| CACCTGCATC | GCCAGTTCGC | GAGTCGG | | | 227 |

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| GATCTAAATC | AAATTAATTG | GTAAAGATA | ACCACAGCGG | GGCCGACATA | 50 |
| AACTCTGACA | AGAAGTTAAC | AACCATATAA | CCTGCACAGG | ACGCGAACAT | 100 |
| GTCTTCTCAT | CCGTATGTCA | CCCAGCAAAA | TACCCGCTG | GCGGACGACA | 150 |
| CCACTCTGAT | GTCCACTACC | GATCTCGCTT | TCCAGCGTCA | TATTGGGGCG | 200 |
| CGCTACGTTG | GGGCGTGGGC | GTAATTGGTC | AATCAGGCGC | GGGGTCAGCG | 250 |
| GATAAACATT | CACCATTTTG | TCGAGATC | | | 278 |

SUBSTITUTE SHEET

61

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1596 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

| | | | | | |
|-------------|-------------|-------------|-------------|-------------|------|
| ATGGCTGACA | TTCTGCTGCT | CGATAATATC | GACTCTTTTA | CGTACAACCT | 50 |
| GGCAGATCAG | TTGCGCAGCA | ATGGGCATAA | CGTGGTGATT | TACCGCAACC | 100 |
| ATATACCGGC | GCAAACCTTA | ATTGAACGCT | TGGCGACCAT | GAGTAATCCG | 150 |
| GTGCTGATGC | TTTCTCCTGG | CCCCGGTG TG | CCGAGCGAAG | CCGGTTGTAT | 200 |
| GCCGGAAC TC | CTCACCCGCT | TGCGTG GCAA | GCTGCCCATT | ATTGGCATT T | 250 |
| GCCTCGGACA | TCAGGCGATT | GTCGAAGCTT | ACGGGGGCTA | TGTCGGTCAG | 300 |
| GCGGGCGAAA | TTCTCCACGG | TAAAGCCTCC | AGCATTGAAC | ATGACGGTCA | 350 |
| GGCGATGTTT | GCCGGATTAA | CAAACCCGCT | GCCGGTGGCG | CGTTATCACT | 400 |
| CGCTGGTTGG | CAGTAACATT | CCGGCCGGTT | TAACCATCAA | CGCCCATTTT | 450 |
| AATGGCATGG | TGATGGCAGT | ACGTCACGAT | GCGGATCGCG | TTTGTGGATT | 500 |
| CCAGTTCCAT | CCGGAATCCA | TTCTCACCAC | CCAGGGCGCT | CGCCTGCTGG | 550 |
| AACAAACGCT | GGCCTGGGCG | CAGCATAAAC | TAGAGCCAGC | CAACACGCTG | 600 |
| CAACCGATT C | TGGA AAAACT | GTATCAGGCG | CAGACGCTTA | GCCAACAAGA | 650 |
| AAGCCACCAG | CTGTTTT CAG | CGGTGGTGCG | TGGCGAGCTG | AAGCCGGAAC | 700 |
| AACTGGCGGC | GGCGCTGGTG | AGCATGAAAA | TTCGCGGTGA | GCACCCGAAC | 750 |
| GAGATCGCCG | GGGCAGCAAC | CGCGCTACTG | GAAAACGCAG | CGCCGTTCCC | 800 |
| GCGCCCGGAT | TATCTGTTTG | CTGATATCGT | CGGTACTGGC | GGTGACGGCA | 850 |
| GCAACAGTAT | CAATATTTCT | ACCGCCAGTG | CGTTTGTCGC | CGCGGCCTGT | 900 |
| GGGCTGAAAG | TGGCGAAACA | CGGCAACCGT | AGCGTCTCCA | GTAAATCTGG | 950 |
| TTCGTCCGAT | CTGCTGGCGG | CGTTCGGTAT | TAATCTTGAT | ATGAACGCCC | 1000 |
| ATAAATCGCG | CCAGGCGCTG | GATGAGTTAG | GTGTATGTTT | CCTCTTTGCG | 1050 |
| CCGAAGTATC | ACACCGGATT | CCGCCACGCG | ATGCCGGTTC | GCCAGCAACT | 1100 |
| GAAAACCCGC | ACCCTGTTCA | ATGTGCTGGG | GCCATTGATT | AACCCGGCGC | 1150 |
| ATCCGCCGCT | GGCGTTAATT | GGTGTTTATA | GTCCGGAAC T | GGTGCTGCCG | 1200 |
| ATTGCCGAAA | CCTTGCGCGT | GCTGGGGTAT | CAACGCGCGG | CGGTGGTGCA | 1250 |
| CAGCGGCGGG | ATGGATGAAG | TTTCATTACA | CGCGCCGACA | ATCGTTGCCG | 1300 |
| AACTGCATGA | CGGCGAAATT | AAAAGCTATC | AGCTCACC GC | AGAAGACTTT | 1350 |

SUBSTITUTE SHEET

62

| | | | | | |
|------------|------------|------------|------------|------------|------|
| GGCCTGACAC | CCTACCACCA | GGAGCAACTG | GCAGGCGGAA | CACCGGAAGA | 1400 |
| AAACCGTGAC | ATTTTAACAC | GTTTGTACAC | AGGTAAAGGC | GACGCCGCCC | 1450 |
| ATGAAGCAGC | CGTCGCTGCG | AACGTCGCCA | TGTTAATGCG | CCTGCATGGC | 1500 |
| CATGAAGATC | TGCAAGCCAA | TGCGCAAACC | GTTCTTGAGG | TACTGCGCAG | 1550 |
| TGGTTCCGCT | TACGACAGAG | TCACCGCACT | GGCGGCACGA | GGGTAA | 1596 |

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2703 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

| | | | | | |
|------------|------------|-------------|------------|-------------|------|
| GACGACTTAG | TTTTGACGGA | ATCAGCATAG | TTAATCACTT | CACTGTGGAA | 50 |
| AATGAGGAAA | TATTATTTTT | TTTGCGCTTC | GTAATTAATG | GTTATAAGGT | 100 |
| CGGCCAGAAA | CCTTTCTAAT | GCAAGCGATG | ACGTTTTTTT | ATGTGTCTGA | 150 |
| ATTTGCACTG | TGTCACAATT | CCAAATCTTT | ATTAACAAC | CACCTAAAAC | 200 |
| GACGCTGATC | CAGCGTGAAT | ACTGGTTTCC | CTTATGTTCA | TCAGATTCAT | 250 |
| TTAAGCAAGG | GTTTCTTCTT | CATTCCTGAT | GAAAGTGCCA | TCTAAAAAGA | 300 |
| TGATCTTAAT | AAATCTATTA | AGAATGAGAT | GGAGCACACT | GGATATTTTA | 350 |
| CTTATGAAAC | TGTTTCACTC | CTTTACTTAA | TTTATAGAGT | TACCTTCCGC | 400 |
| TTTTTTGAAA | TACGCAACGG | CCATTTTTTG | CACTTAGATA | CAGATTTTCT | 450 |
| GCGCTGTATT | GCATTGATTT | GATGCTAATC | CTGTGGTTTG | CACTAGCTTT | 500 |
| AAGTGGTTGA | GATCACATTT | CCTTGCTCAT | CCCCGCAACT | CCTCCCTGCC | 550 |
| TAATCCCCCG | CAGGATGAGG | AAGGTCAACA | TCGAGCCTGG | CAAAC TAGCG | 600 |
| ATAACGTTGT | GTTGAAAATC | TAAGAAAAGT | GGAATCCTA | TGTCACAACC | 650 |
| TATTTTTAAC | GATAAGCAAT | TTCAGGAAGC | GCTTTCACGT | CAGTGGCAGC | 700 |
| GTTATGGCTT | AAATTCTGCG | GCTGAAATGA | CTCCTCGCCA | GTGGTGGCTA | 750 |
| GCAGTGAGTG | AAGCACTGGC | CGAAATGCTG | CGTGCTCAGC | CATTGCGCAA | 800 |
| GCCGGTGGCG | AATCAGCGAC | ATGTAACTA | CATCTCAATG | GAGTTTTTGA | 850 |
| TTGGTCGCCT | GACGGGCAAC | AACCTGTTGA | ATCTCGGCTG | GTATCAGGAT | 900 |
| GTACAGGATT | CGTTGAAGGC | TTATGACATC | AATCTGACGG | ACCTGCTGGA | 950 |
| AGAAGAGATC | GACCCGGCGC | TGGGTAACGG | TGGTCTGGGA | CGTCTGGCGG | 1000 |
| CGTGCTTCCT | CGACTCAATG | GCAACTGTCTG | GTCAGTCTGC | GACGGGTAC | 1050 |

SUBSTITUTE SHEET

63

| | | | | | |
|-------------|------------|------------|-------------|------------|------|
| GGTCTGAACT | ATCAATATGG | TTTGTTCCGC | CAGTCTTTTG | TCGATGGCAA | 1100 |
| ACAGGTTGAA | GCGCCGGATG | ACTGGCATCG | CAGTAACTAC | CCGTGGTTCC | 1150 |
| GCCACAACGA | AGCACTGGAT | GTGCAGGTAG | GGATTGGCGG | TAAAGTGACG | 1200 |
| AAAGACGGAC | GCTGGGAGCC | GGAGTTTACC | ATTACCGGTC | AAGCGTGGGA | 1250 |
| TCTCCCCGTT | GTCGGCTATC | GTAATGGCGT | GGCGCAGCCG | CTGCGTCTGT | 1300 |
| GGCAGGCGAC | GCACGCGCAT | CCGTTTGATC | TGACTAAATT | TAACGACGGT | 1350 |
| GATTTCTTGC | GTGCCGAACA | GCAGGGCATC | AATGCGGAAA | AACTGACCAA | 1400 |
| AGTTCTCTAT | CCAAACGACA | ACCATACTGC | CGGTAAAAAG | CTGCGCCTGA | 1450 |
| TGCAGCAATA | CTTCCAGTGT | GCCTGTTCCG | TAGCGGATAT | TTTGCGTCGC | 1500 |
| CATCATCTGG | CGGGGCGTGA | ACTGCACGAA | CTGGCGGATT | ACTAAGTTAT | 1550 |
| TCAGCTGAAC | GATACCCACC | CAACTATCGC | GATTCCAGAA | CTGCTGCGCG | 1600 |
| TGCTGATCGA | TGAGCACCAG | ATGAGCTGGG | ATGACGCTTG | GGCCATTACC | 1650 |
| AGCAAAACTT | TCGCTTACAC | CAACCATACC | CTGATGCCAG | AAGCGCTGGA | 1700 |
| ACGCTGGGAT | GTGAAACTGG | TGAAAGGCTT | ACTGCCGCGC | CACATGCAGA | 1750 |
| TTATTAACGA | AATTAATACT | CGCTTTAAAA | CGCTGGTAGA | GAAAACCTGG | 1800 |
| CCGGGCGATG | AAAAAGTGTG | GGCCAAACTG | GCGGTGGTGC | ACGACAAACA | 1850 |
| AGTGCAATATG | GCGAACCTGT | GTGTGGTTGG | CGGTTTCGCG | GTGAACGGTG | 1900 |
| TTGCGGCGCT | GCACTCGGAT | CTGGTGGTGA | AAGATCTGTT | CCCGBAATAT | 1950 |
| CACCAGCTAT | GGCCGAACAA | ATTCCATAAC | GTCACCAACG | GTATTACCCC | 2000 |
| ACGTCGCTGG | ATCAAACAGT | GCAACCCGGC | ACTGGCGGCT | CTGTTGGATA | 2050 |
| AATCACTGCA | AAAAGAGTGG | GCTAACGATC | TCGATCAGCT | GATCAATCTG | 2100 |
| GTTAAATTGG | CTGATGATGC | GAAATTCCGT | CAGCTTTATC | GCGTGATCAA | 2150 |
| GCAGGCGAAT | AAAGTCCGTC | TGGCGGAGTT | TGTGAAAGTT | CGTACCGGTA | 2200 |
| TTGACATCAA | TCCACAGGCG | ATTTTCGATA | TTCAGATCAA | ACGTTTGCAC | 2250 |
| GAGTACAAAC | GCCAGCACCT | GAATCTGCTG | CGTATTCTGG | CGTTGTACAA | 2300 |
| AGAAATTTCGT | GAAAACCCGC | AGGCTGATCG | CGTACCGCGC | GTCTTCCTCT | 2350 |
| TCGGCGCGAA | AGCGGCACCG | GGCTACTACC | TGGCTAAGAA | TATTATCTTT | 2400 |
| GCGATCAACA | AAGTGGCTGA | CGTGATCAAC | AACGATCCGC | TGGTTGGCGA | 2450 |
| TAAGTTGAAG | GTGGTGTTC | TGCCGGATTA | TTGCGTTTCG | GCGGCGGAAA | 2500 |
| AACTGATCCC | GGCGGCGGAT | ATCTCCGAAC | AAATTTTCGAC | TGCAGGTAAA | 2550 |
| GAAGCTTCCG | GTACCGGCAA | TATGAAACTG | GCGCTCAATG | GTGCGCTTAC | 2600 |
| TGTCGGTACG | CTGGATGGGG | CGAACGTTGA | AATCGCCGAG | AAAGTCGGTG | 2650 |
| AAGAAAATAT | CTTTATTTTT | GGTCATACGG | TCAAACAAGT | GAAGGCAATC | 2700 |
| GAC | | | | | 2703 |

SUBSTITUTE SHEET

64

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1391 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

| | | | | | |
|-------------|------------|------------|------------|------------|------|
| AGAGAAGCCT | GTCGGCACCG | TCTGGTTTGC | TTTTGCCACT | GCCCCGCGTG | 50 |
| AAGGCATTAC | CCGGCGGGAT | GCTTCAGCGG | CGACCGTGAT | GCGGTGCGTC | 100 |
| GTCAGGCTAC | TGCGTATGCA | TTGCAGACCT | TGTGGCAACA | ATTTCTACAA | 150 |
| AACACTTGAT | ACTGTATGAG | CATACAGTAT | AATTGCTTCA | ACAGAACATA | 200 |
| TTGACTATCC | GGTATTACCC | GGCATGACAG | GAGTAAAAAT | GGCTATCGAC | 250 |
| GAAAACAAAC | AGAAAGCGTT | GGCGGCAGCA | CTGGGCCAGA | TTGAGAAACA | 300 |
| ATTTGGTAAA | GGCTCCATCA | TGCGCCTGGG | TGAAGACCGT | TCCATGGATG | 350 |
| TGGAAACCAT | CTCTACCGGT | TCGCTTTTAC | TGGATATCGC | GCTTGGGGCA | 400 |
| GGTGGTCTGC | CGATGGGCCG | TATCGTCGAA | ATCTACGGAC | CGGAATCTTC | 450 |
| CGGTAAAACC | ACGCTGACGC | TGCAGGTGAT | CGCCGCAGCG | CAGCGTGAAG | 500 |
| GTAAACCTG | TGCGTTTATC | GATGCTGAAC | ACGCGCTGGA | CCCAATCTAC | 550 |
| GCACGTAAAC | TGGGCGTCGA | TATCGACAAC | CTGCTGTGCT | CCCAGCCGGA | 600 |
| CACCGGCGAG | CAGGCACTGG | AAATCTGTGA | CGCCCTGGCG | CGTTCTGGCG | 650 |
| CAGTAGACGT | TATCGTCGTT | GACTCCGTGG | CGGCACTGAC | GCCGAAAGCG | 700 |
| GAAATCGAAG | GCGAAATCGG | CGACTCTCAC | ATGGGCCTTG | CGGCACGTAT | 750 |
| GATGAGCCAG | GCGATGCGTA | AGCTGGCGGG | TAACCTGAAG | CAGTCCAACA | 800 |
| CGCTGCTGAT | CTTCATCAAC | CAGATCCGTA | TGAAAATTGG | TGTGATGTTT | 850 |
| GGTAACCCCG | AAACCACTAC | CGGTGGTAAC | GCGCTGAAAT | TCTACGCCTC | 900 |
| TGTTTCGTCTC | GACATCCGTC | GTATCGGCGC | GGTGAAAGAG | GGCGAAAACG | 950 |
| TGGTGGGTAG | CGAAACCCGC | GTGAAAGTGG | TGAAGAACAA | AATCGCTGCG | 1000 |
| CCGTTTAAAC | AGGCTGAATT | CCAGATCCTC | TACGGCGAAG | GTATCAACTT | 1050 |
| CTACGGCGAA | CTGGTTGACC | TGGGCGTAAA | AGAGAAGCTG | ATCGAGAAAG | 1100 |
| CAGGCGCGTG | GTACAGCTAC | AAAGGTGAGA | AGATCGGTCA | GGGTAAAGCG | 1150 |
| AATGCGACTG | CCTGGCTGAA | AGATAACCCG | GAAACCGCGA | AAGAGATCGA | 1200 |
| GAAGAAAGTA | CGTGAGTTGC | TGCTGAGCAA | CCCGAACTCA | ACGCCGGATT | 1250 |
| TCTCTGTAGA | TGATAGCGAA | GGCGTAGCAG | AAACTAACGA | AGATTTTAA | 1300 |

SUBSTITUTE SHEET

65

TCGTCTTGTT TGATACACAA GGGTCGCATC TCGGGCCCTT TTGCTTTTTT 1350
 AAGTTGTAAG GATATGCCAT GACAGAATCA ACATCCCGTC G 1391

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGCCAGGAA GGCGGCATTC GGCTGGGTCA GAGTGACCTG CAGCGTGGTG 50
 TCGTTCAGCG CTTTCACCCC CAACGTCTCG GGTCCCTTTT GCCCGAGGGC 100
 AATCTCGCGG GCGTTGGCGA TATGCATATT GCCAGGGTAG CTCGCGTAGG 150
 GGGAGGCTGT TGCCGGCGAG ACCAGCCGTT GCCAGCTCCA GACGATATCC 200
 TCGCCTGTAA TGGCCGTGCC GTCAGACCAG GTCAGACC 238

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAGCGTAATG CGCCGCGGCA TAACGGCGCC ACTATCGACA GTCAGTTCGT 50
 CAGCCTGCAG CCTGGGCTGA ATCTGGGACC ATGGCGCCTG CCGAACTACA 100
 GCACCTATAG CCACAGCGAT AACAACAGCC GCTGGGAGTC GGTTTACTCC 150
 TATCTTGCCC GCGATATTCA CACCCTACGC AGCCAGCTGG TGGTCGGTAA 200
 TACGTATACC TCTTCCGGCA TTTTCGACAG TTTGAGTTTT ACCGGTCTGC 250
 AGCTCAGTTC GACAAAGAGA TGCTGCCGGA TAGCCTGCAT GCTTTGCGCC 300
 GACGATTCGA GGGATCGCGC GCACCACCGC GGAGGTCTCG GTTTATCAGA 350

SUBSTITUTE SHEET

66

ATGGTTACAG CATTTATAAA ACCACCGTCG CTACC

385

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CTCTATATTC | AGGACGAACA | TATCTGGACC | TCTGGCGGGG | TCAGTTCCGG | 50 |
| CTTTGATCGC | CCTGCACCCG | CAGCGGGTGA | TCGCCCCTCA | TCTGCTACTG | 100 |
| CGGCGCTGCA | ACAGGCGACG | ATCGATGACG | TTATTCCTGG | CCAGCAAACA | 150 |
| GCAGACCAAT | TAAGGTCTGA | TAGTGGCTCT | CTTCCTCCGG | CGCGCGACGG | 200 |
| TCCAGGCGGC | TCAACAGTTT | GGTGCATAGC | GCTTTGCGGT | TGAGATGACG | 250 |
| CCCTTCGTTA | AGAATATCCA | TCACGATCTC | CGTCCATGGA | GAGTAGCGTT | 300 |
| TATTCCAGAA | TAGGGTTTTT | CAGGATCTCA | TGGATCTGCG | CCTGCTTATC | 350 |
| GCTATTTTGT | AACCAGATCG | CATAAAGTGG | ACGGGATAAC | GTAGCGCTGT | 400 |
| CCATGACCGT | ATGTAACCCA | TGCTTCTCTT | TCGCCCAGCG | AGCAGGTAGC | 450 |
| CAACAGCAGC | CG | | | | 462 |

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 730 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| GCTGACCGCT | AAACTGGGTT | ACCCGATCAC | TGACGATCTG | GACATCTACA | 50 |
| CCCGTCTGGG | CGGCATGGTT | TGGCGCGCTG | ACTCCAAAGG | CAACTACGCT | 100 |
| TCAACCGGCG | TTTCCCGTAG | CGAACACGAC | ACTGGCGTTT | CCCCAGTATT | 150 |
| TGCTGGCGGC | GTAGAGTGGG | CTGTTACTCG | TGACATCGCT | ACCCGTCTGG | 200 |

SUBSTITUTE SHEET

67

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| AATACCAGTG | GGTTAACAAC | ATCGGCGACG | CGGGCACTGT | GGGTACCCGT | 250 |
| CCTGATAACG | GCATGCTGAG | CCTGGGCGTT | TCCTACCGCT | TCGGTCAGGA | 300 |
| AGATGCTGCA | CCGGTTGTTG | CTCCGGCTCC | GGCTCCGGCT | CCGGAAGTGG | 350 |
| CTACCAAGCA | CTTCACCCTG | AAGTCTGACG | TTCTGTTCAA | CTTCAACAAA | 400 |
| GCTACCCTGA | AACCGGAAGG | TCAGCAGGCT | CTGGATCAGC | TGTACACTCA | 450 |
| GCTGAGCAAC | ATGGATCCGA | AAGACGGTTC | CGCTGTTGTT | CTGGGCTACA | 500 |
| CCGACCGCAT | CGGTTCCGAA | GCTTACAACC | AGCAGCTGTC | TGAGAAACGT | 550 |
| GCTCAGTCCG | TTGTTGACTA | CCTGGTTGCT | AAAGGCATCC | CGGCTGGCAA | 600 |
| AATCTCCGCT | CGCGGCATGG | GTGAATCCAA | CCCGGTTACT | GGCAACACCT | 650 |
| GTGACAACGT | GAAAGCTCGC | GCTGCCCTGA | TCGATTGCCT | GGCTCCGGAT | 700 |
| CGTCGTGTAG | AGATCGAAGT | TAAAGGTATC | | | 730 |

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

| | | | | | |
|------------|------------|-------------|------------|------------|-----|
| CGCTACTGTT | TAAATCTCAT | TTGAAACATC | GCAAAGTCAG | TGAACCACAT | 50 |
| ATTCGAGGAT | GGCATGCACT | AGAAAATATT | AATAAGATTT | TAGCGAAACC | 100 |
| TAATCAGCGC | AATATCGCTT | AATTATTTTA | GGTATGTTCT | CTTCTATCCT | 150 |
| ACAGTCACGA | GGCAGTGTCT | AACCTTGATCC | TCATTTTATT | AATCACATGA | 200 |
| CCAATGGTAT | AAGCGTCGTC | ACATA | | | 225 |

SUBSTITUTE SHEET

68

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ACATTTTAAA | TAGGAAGCCA | CCTGATAACA | TCCCCGCAGT | TGGATCATCA | 50 |
| GATTTATAGC | GGCATTGTGT | ATCCGCTAGA | TAAAAGCAGT | CCAACGATCC | 100 |
| CGCCAATTGT | TAGATGAAAT | TGGACTATTC | TTTTTATTTG | CTCCGCTTTA | 150 |
| TCACAGTGGT | TTTCGCTTTG | CCGCCCCTGT | GCGCCAACAG | CTAAGAACAC | 200 |
| GCACGCTCTT | TAATGTGTTA | GGCCCATTA | TTAATCCAGC | GCGTTCCGCC | 250 |
| TTTAGCATTA | ATTGGTGTTT | ATAGTCCTGA | ATTATTAATG | CCTATTGCAG | 300 |
| ATACCTTAAA | TGTCTTGGGC | TACAAACGTG | CGGCAGTGGT | CCATAGTGGT | 350 |
| GGAATGGATG | AAGTGTCATT | ACATGCTCCC | ACACAAGTGG | CTGAGTTACA | 400 |
| CA | | | | | 402 |

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CTGAAACGCA | TTTATGCGGG | AGTCAGTGAA | ATCATCACTC | AATTTTCACC | 50 |
| CGATGTATTT | TCTGTTGAAC | AAGTCTTTAT | GGCAAAAAAT | GCAGACTCAG | 100 |
| CATTAAATT | AGGCCAAGCA | AGAGGTGTGG | CGATTTTAGC | GGCAGTCAAT | 150 |
| AATGATC | | | | | 157 |

SUBSTITUTE SHEET

69

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

| | | | | | |
|------------|------------|------------|------------|------------|------|
| TTTCTCTTTA | AAATCAATTC | TAAAGAAAT | TATTAATAAT | TAAGTGATA | 50 |
| CTGTATGATT | ATACAGTATA | ATGAGTTTCA | ACAAGCAAAA | TCATATACGT | 100 |
| TTTAATGGTA | GTGACCCATC | TTTATGCTTC | ACTGCCCAGA | GGGAGATAAC | 150 |
| ATGGCTATTG | ATGAAAACAA | ACAAAAGCA | TTGGCCGCAG | CACTTGGTCA | 200 |
| AATTGAAAAG | CAATTTGGTA | AAGGTTCTAT | CATGCGTCTG | GGCGAAGACC | 250 |
| GTTCCATGAA | CGTAGAAACT | ATCTCTACAG | GATCTTTATC | ATTAGACGTT | 300 |
| GCTTTAGGTG | CAGGTGGATT | GCCACGTGGC | CGTATTGTTG | AAATCTATGG | 350 |
| CCCTGAATCT | TCTGGTAAAA | CAACCTTGAC | TCTACAAGTT | ATTGCCTCTG | 400 |
| CTCAGCGTGA | AGGAAAAATT | TGTGCATTTA | TTGATGCTGA | ACATGCATTA | 450 |
| GACCCAATTT | ATGCTCAAAA | GCTAGGTGTC | GATATCGATA | ATCTACTCTG | 500 |
| CTCTCAACCT | GACACAGGTG | AACAAGCTCT | GGAAATTTGT | GATGCATTAT | 550 |
| CTCGCTCTGG | TGCGGTCGAT | GTTATTGTCG | TGGACTCCGT | GGCAGCATTA | 600 |
| ACACCAAAG | CTGAAATTGA | AGGTGAAATT | GGTGATTAC | ACGTTGGTTT | 650 |
| AGCCGCACGT | ATGATGAGCC | AAGCTATGCG | TAAACTAGCG | GGTAACCTTA | 700 |
| AAAACCTCTA | TACACTGCTG | ATTTTCATTA | ACCAAATTCG | TATGAAAATC | 750 |
| GGTGTTATGT | TTGGTAACCC | AGAAACCACG | ACCGGTGGTA | ATGCGCTTAA | 800 |
| ATTCTATGCT | TCTGTTTCGT | TAGACATTCG | TCGCATTGGC | TCTGTCAAAA | 850 |
| ATGGTGATGA | AGTCATTGGT | AGTGAGACTC | GCGTTAAAGT | TGTTAAAAAT | 900 |
| AAAGTGGCTG | CACCGTTTAA | ACAAGCTGAA | TTCCAAATTA | TGTACGGTGA | 950 |
| AGGTATTAAT | ACCTATGGCG | AACTGATTGA | TTTAGGTGTT | AAACATAAGT | 1000 |
| TAGTAGAGAA | AGCAGGTGCT | TGGTATAGCT | ACAATGGCGA | AAAAATTGGT | 1050 |
| CAAGGTAAAG | CTAACGCAAC | CAATTACTTA | AAAGAACATC | CTGAAATGTA | 1100 |
| CAATGAGTTA | AACACTAAAT | TGCGTGAAAT | GTTGTTAAAT | CATGCTGGTG | 1150 |
| AATTCACAAG | TGCTGCGGAT | TTTGCAGGTG | AAGAGTCAGA | CAGTGATGCT | 1200 |
| GACGACACAA | AAGAGTAATT | AGCTGGTTGT | CATGCTGTTT | GTGTGAAAAT | 1250 |
| AGACCTTAAA | TCATTGGCTA | TTATCACGAC | AGCATCCCAT | AGAATAACTT | 1300 |

SUBSTITUTE SHEET

70

GTTTGTATAA ATTTTATTCA GATGGCAAAG GAAGCCTTAA AAAAGCTT 1348

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2167 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

| | | | | | |
|------------|------------|------------|------------|------------|------|
| GGTACCGCTG | GCCGAGCATC | TGCTCGATCA | CCACCAGCCG | GGCGACGGGA | 50 |
| ACTGCACGAT | CTACCTGGCG | AGCCTGGAGC | ACGAGCGGGT | TCGCTTCGTA | 100 |
| CGGCGCTGAG | CGACAGTCAC | AGGAGAGGAA | ACGGATGGGA | TCGCACCAGG | 150 |
| AGCGGCCGCT | GATCGGCCTG | CTGTTCTCCG | AAACCGGCGT | CACCGCCGAT | 200 |
| ATCGAGCGCT | CGCACGCGTA | TGGCGCATTG | CTCGCGGTCG | AGCAACTGAA | 250 |
| CCGCGAGGGC | GGCGTCGGCG | GTCGCCCAGT | CGAAACGCTG | TCCCAGGACC | 300 |
| CCGGCGGCCA | CCCGGACCGC | TATCGGCTGT | GCGCCGAGGA | CTTCATTTCG | 350 |
| AACCGGGGGG | TACGGTTCCT | CGTGGGCTGC | TACATGTCGC | ACACGCGCAA | 400 |
| GGCGGTGATG | CCGGTGGTCG | AGCGCGCCGA | CGCGCTGCTC | TGCTACCCGA | 450 |
| CCCCCTACGA | GGGCTTCGAG | TATTCGCCGA | ACATCGTCTA | CGGCGGTCCG | 500 |
| GCGCCGAACC | AGAACAGTGC | GCCGCTGGCG | GCGTACCTGA | TTCGCCACTA | 550 |
| CGGCGAGCGG | GTGGTGTTCA | TCGGCTCGGA | CTACATCTAT | CCGCGGGAAA | 600 |
| GCAACCATGT | GATGCGCCAC | CTGTATCGCC | AGCACGGCGG | CACGGTGCTC | 650 |
| GAGGAAATCT | ACATTCCGCT | GTATCCCTCC | GACGACGACT | TGCAGCGCGC | 700 |
| CGTCGAGCGC | ATCTACCAGG | CGCGCGCCGA | CGTGGTCTTC | TCCACCGTGG | 750 |
| TGGGCACCGG | CACCGCCGAG | CTGTATCGCG | CCATCGCCCC | TCGCTACGGC | 800 |
| GACGGCAGGC | GGCCGCCGAT | CGCCAGCCTG | ACCACCAGCG | AGGCGGAGGT | 850 |
| GGCGAAGATG | GAGAGTGACG | TGGCAGAGGG | GCAGGTGGTG | GTCGCGCCTT | 900 |
| ACTTCTCCAG | CATCGATACG | CCCGCCAGCC | GGGCCTTCGT | CCAGGCCTGC | 950 |
| CATGGTTTCT | TCCCGGAGAA | CGCGACCATC | ACCGCCTGGG | CCGAGGCGGC | 1000 |
| CTACTGGCAG | ACCTTGTTGC | TCGGCCGCGC | CGCGCAGGCC | GCAGGCAACT | 1050 |
| GGCGGGTGGA | AGACGTGCAG | CGGCACCTGT | ACGACATCGA | CATCGACGCG | 1100 |
| CCACAGGGGC | CGGTCCGGGT | GGAGCGCCAG | AACAACCACA | GCCGCCTGTC | 1150 |
| TTCGCGCATC | GCGGAAATCG | ATGCGCGCGG | CGTGTTCAG | GTCCGCTGGC | 1200 |
| AGTCGCCCCA | ACCGATTTCG | CCCGACCCTT | ATGTCGTCGT | GCATAACCTC | 1250 |

SUBSTITUTE SHEET

71

| | | | | | |
|------------|------------|------------|------------|------------|------|
| GACGACTGGT | CCGCCAGCAT | GCGCGGGGGA | CCGCTCCCAT | GAGCGCCAAC | 1300 |
| TCGCTGCTCG | GCAGCCTGCG | CGAGTTGCAG | GTGCTGGTCC | TCAACCCGCC | 1350 |
| GGGGGAGGTC | AGCGACGCCC | TGGTCTTGCA | GCTGATCCGC | ATCGGTTGTT | 1400 |
| CGGTGCGCCA | GTGCTGGCCG | CCGCCGGAAG | CCTTCGACGT | GCCGGTGGAC | 1450 |
| GTGGTCTTCA | CCAGCATTTT | CCAGAATGGC | CACCACGACG | AGATCGCTGC | 1500 |
| GCTGCTCGCC | GCCGGGACTC | CGCGCACTAC | CCTGGTGGCG | CTGGTGGAGT | 1550 |
| ACGAAAGCCC | CGCGGTGCTC | TCGCAGATCA | TCGAGCTGGA | GTGCCACGGC | 1600 |
| GTGATCACCC | AGCCGCTCGA | TGCCACCCGG | GTGCTGCCTG | TGCTGGTATC | 1650 |
| GGCGCGGCGC | ATCAGCGAGG | AAATGGCGAA | GCTGAAGCAG | AAGACCGAGC | 1700 |
| AGCTCCAGGA | CCGCATCGCC | GGCCAGGCCC | GGATCAACCA | GGCCAAGGTG | 1750 |
| TTGCTGATGC | AGCGCCATGG | CTGGGACGAG | CGCGAGGCGC | ACCAGCACCT | 1800 |
| GTGCGGGGAA | GCGATGAAGC | GGCGCGAGCC | GATCCTGAAG | ATCGCTCAGG | 1850 |
| AGTTGCTGGG | AAACGAGCCG | TCCGCCTGAG | CGATCCGGGC | CGACCAGAAC | 1900 |
| AATAACAAGA | GGGGTATCGT | CATCATGCTG | GGACTGGTTC | TGCTGTACGT | 1950 |
| TGGCGCGGTG | CTGTTTCTCA | ATGCCGTCTG | GTTGCTGGGC | AAGATCAGCG | 2000 |
| GTGCGGAGGT | GGCGGTGATC | AACTTCCTGG | TCGGCGTGCT | GAGCGCCTGC | 2050 |
| GTCGCGTTCT | ACCTGATCTT | TTCCGCAGCA | GCCGGGCAGG | GCTCGCTGAA | 2100 |
| GGCCGGAGCG | CTGACCCTGC | TATTCGCTTT | TACCTATCTG | TGGGTGGCCG | 2150 |
| CCAACCAGTT | CCTCGAG | | | | 2167 |

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| GAATTCCCGG | GAGTCCCGA | CGCAGCCACC | CCCAAAACAC | TGCTAAGGGA | 50 |
| GCGCCTCGCA | GGGCTCCTGA | GGAGATAGAC | CATGCCATTT | GGCAAGCCAC | 100 |
| TGGTGGGCAC | CTTGCTCGCC | TCGCTGACGC | TGCTGGGCCT | GGCCACCGCT | 150 |
| CACGCCAAGG | ACGACATGAA | AGCCGCCGAG | CAATACCAGG | GTGCCGCTTC | 200 |
| CGCCGTCGAT | CCCGCTCACG | TGGTGCGCAC | CAACGGCGCT | CCCGACATGA | 250 |
| GTGAAAGCGA | GTTCAACGAG | GCCAAGCAGA | TCTACTTCCA | ACGCTGCGCC | 300 |
| GGTTGCCACG | GCGTCCTGCG | CAAGGGCGCC | ACCGGCAAGC | CGCTGACCCC | 350 |

SUBSTITUTE SHEET

72

| | | | | | |
|------------|-------------|-------------|-------------|------------|------|
| GGACATCACC | CAGCAACGCG | GCCAGCAATA | CCTGGAAGCG | CTGATCACCT | 400 |
| ACGGCACCCC | GCTGGGCATG | CCGAAC TGGG | GCAGCTCCGG | CGAGCTGAGC | 450 |
| AAGGAACAGA | TCACCCTGAT | GGCCAAGTAC | ATCCAGCACA | CCCCGCCGCA | 500 |
| ACCGCCGGAG | TGGGGCATGC | CGGAGATGCG | CGAATCGTGG | AAGGTGCTGG | 550 |
| TGAAGCCGGA | GGACCGGCCG | AAGAAACAGC | TCAACGACCT | CGACCTGCCC | 600 |
| AACCTGTTCT | CGGTGACCCT | GCGCGACGCC | GGGCAGATCG | CCCTGGTCGA | 650 |
| CGGCGACAGC | AAAAAGATCG | TCAAGGTCAT | CGATACCGGC | TATGCCGTGC | 700 |
| ATATCTCGCG | GATGTCCGCT | TCCGGCCGCT | ACCTGCTGGT | GATCGGCCGC | 750 |
| GACGCGCGGA | TCGACATGAT | CGACCTGTGG | GCCAAGGAGC | CGACCAAGGT | 800 |
| CGCCGAGATC | AAGATCGGCA | TCGAGGCGCG | CTCGGTGGAA | AGCTCCAAGT | 850 |
| TCAAGGGCTA | CGAGGACCGC | TACACCATCG | CCGGCGCCTA | CTGGCCGCCG | 900 |
| CAGTTCGCGA | TCATGGACGG | CGAGACCCTG | GAACCGAAGC | AGATCGTCTC | 950 |
| CACCCGCGGC | ATGACCGTAG | ACACCCAGAC | CTACCACCCG | GAACCGCGCG | 1000 |
| TGGCGGCGAT | CATCGCCTCC | CACGAGCACC | CCGAGTTCAT | CGTCAACGTG | 1050 |
| AAGGAGACCG | GCAAGGTCCT | GCTGGTCAAC | TACAAGGATA | TCGACAACCT | 1100 |
| CACCGTCACC | AGCATCGGTG | CGGCGCCGTT | CCTCCACGAC | GGCGGCTGGG | 1150 |
| ACAGCAGCCA | CCGCTACTTC | ATGACCGCCG | CCAACAAC TC | CAACAAGGTT | 1200 |
| GCCGTGATCG | ACTCCAAGGA | CCGTGCGCTG | TCGGCCCTGG | TCGACGTGCG | 1250 |
| CAAGACCCCG | CACCCGGGGC | GTGGCGCCAA | CTTCGTGCAT | CCCAAGTACG | 1300 |
| GCCCGGTGTG | GAGCACCAGC | CACCTGGGCG | ACGGCAGCAT | CTCGCTGATC | 1350 |
| GGCACCGATC | CGAAGAACCA | TCCGCAGTAC | GCCTGGAAGA | AAGTCGCCGA | 1400 |
| ACTACAGGGC | CAGGGCGGCG | GCTCGCTGTT | CATCAAGACC | CATCCGAAGT | 1450 |
| CCTCGCACCT | CTACGTCGAC | ACCACCTTCA | ACCCCGACGC | CAGGATCAGC | 1500 |
| CAGAGCGTCG | CGGTGTTCTGA | CCTGAAGAAC | CTCGACGCCA | AGTACCAGGT | 1550 |
| GCTGCCGATC | GCCGAATGGG | CCGATCTCGG | CGAAGGCGCC | AAGCGGGTGG | 1600 |
| TGCAGCCCGA | GTACAACAAG | CGCGGCGATG | AAGTCTGGTT | CTCGGTGTGG | 1650 |
| AACGGCAAGA | ACGACAGCTC | CGCGCTGGTG | GTGGTGGACG | ACAAGACCCT | 1700 |
| GAAGCTCAAG | GCCGTGGTCA | AGGACCCGCG | GCTGATCACC | CCGACCGGTA | 1750 |
| AGTTCAACGT | CTACAACACC | CAGCACGACG | TGTACTGAGA | CCCGCGTGCG | 1800 |
| GGGCACGCCC | CGCACGCTCC | CCCCTACGAG | GAACCGTGAT | GAAACCGTAC | 1850 |
| GCACTGCTTT | CGCTGCTCGC | CA | | | 1872 |

SUBSTITUTE SHEET

73

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3451 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

| | | | | | |
|-------------|------------|------------|------------|-------------|------|
| TCGAGACGGG | AAGCCACTCT | CTACGAGAAG | ACAGAAGCCC | CTCACAGAGG | 50 |
| CCTCTGTCTA | CGCCTACTAA | AGCTCGGCTT | ATTCATATGT | ATTTATATTC | 100 |
| TTTCAATAGA | TCACTCAGCG | CTATTTTAAG | TTCACCCTCT | GTAAGTTCAC | 150 |
| CTGGGCGCTC | TTTCTTTTCT | TCGGTAAAGC | TGTCGGCCAG | ACCAAACATT | 200 |
| AAACTCAAGC | ATCTCCCAAG | CGATGCATCA | TCTTGGGCCA | GCATCCCTGA | 250 |
| ATCGCGCGTC | GGACCTCCAA | GTCTTAAAAA | ATTCTTCGCT | GAAGGTTTTTC | 300 |
| CCATCAATCG | ATGAGGCTAA | TAGCTTCTTT | GCAATATCTA | TCATTTCCAT | 350 |
| GCTCACCTTA | AAGCACCTCA | TTTTTCATGT | AAAAATTGTA | TTGATCCGTG | 400 |
| CCAGACTCAA | TCCTCCACCC | AGAAACAAAC | ATCCCATCCT | CTCCAATGAT | 450 |
| AACAACAATA | TTAGTCCTGG | CATTGTAATG | TACTTTTGAG | TTTACTTCGG | 500 |
| AGTGGAAGT | CCCTTTTTCT | ACGGTTGCAG | GATCAGCAAG | GTGCTCAAGA | 550 |
| ATTTTATCCC | TAAACTCTGC | AAGCGTTCCA | TTGTTGGCGC | TTTTTTCACC | 600 |
| CAGCCCAAAA | TCATATTTGT | GGCTATCAAA | TTTTTTCTGT | AGTTGCCTCC | 650 |
| GTGTGAAGAT | ACCACTATCA | AGAGGACTAC | TGAGCATTAC | ATAAACAGGT | 700 |
| TTGACTCCAG | AATCCGCCGG | GAAATCACG | ATCAGATCGT | TTAGGTCCAG | 750 |
| TAGCATTCCC | GGATAGGACT | CCGGGCCGGT | CTTCAACGGT | GTGAGGGCCG | 800 |
| CTCCCTCATA | TACCGGCACC | GGCTTCGGTA | TGACCGGAGT | GGTACTCGAA | 850 |
| GGGTTCCTGGT | TTCTTGAGG | ACTCGCCGGC | GTCCAAGTCA | GGATCAGTGG | 900 |
| CGGCGCTTCT | GCGACCGTAG | AGGGAACCGT | AACCTCGTAC | AGTCCTGTTG | 950 |
| CGGCGTTATA | GGCCCCATCC | GGACCGGAAC | GCTTTCGGAA | CGCTCACACC | 1000 |
| ATCGGTCTGA | CCACCGAAAG | GTCGTCGTGT | TGCCTCGCGC | CTCGTTGGTC | 1050 |
| AGGCGCATCG | GCAGATCGAC | GGTACCGCTG | GCTTTTGCAA | CCGCGTTCAG | 1100 |
| GTTTACGCTT | GGGGGAAGCC | CCAATTTAGC | GGCATCCATG | CCCAGGGCGT | 1150 |
| AACGAACGCT | ATCGGGCGTT | TGGTCCTGCC | ATTGCTCGGC | AGTCCGGGAG | 1200 |
| AGTAGGTCAG | ACTGGCAAGC | CACGGCCATC | ACCGAGGTGC | TGAAGCCAGG | 1250 |
| ACCGCCAGGA | CGGCAATCGC | ATCGGAGATC | GCTTGAGCAA | GGGATGCGGC | 1300 |

SUBSTITUTE SHEET

74

| | | | | | |
|------------|-------------|------------|------------|------------|------|
| GCCTGTGCGA | CCTGGATCAG | ACCCCGCTGC | GGCGGTGGCG | CACCCGCTGC | 1350 |
| CATTGGCTGG | CATGGCATAA | GTATTGGCAG | CCCTGATCGC | CGCTTGACGA | 1400 |
| GCGATTTCCT | TGCGCCTTGC | CGTTTCGGCG | TTCAGCTTGT | CCAGCCGTGC | 1450 |
| TTGCAGGCTG | GCGATTTTCAT | CCACTAGGTA | GGACATCGGC | GTTGTAGGTT | 1500 |
| GCCTTTTGT | TCTCCAGTGC | ATTGGGTGCC | TTGGCAATCA | AGGCATTGTT | 1550 |
| TGCAGTCTGC | AATTCTTCTT | ATTGCGATCG | CCTGCGTAAG | GAGTTGAGTA | 1600 |
| GCGCGTTCAA | GCCACTGCTC | TGGCGTTGGA | TTGGTCAGTT | GAGGCAAAGC | 1650 |
| ATTCCCAGCC | TGGTCAAGCT | CGGACTGCAC | TTTTTTCTCG | ACATTGTCCT | 1700 |
| TCCTGGCCTT | GTAGTCCGCC | TCCACCTCAG | CAGCGGCTCG | CTGGGCTTCT | 1750 |
| GCTTCCAATG | ACCGGGCTTT | ATTCTCCAGC | TCTTGAGACG | TTTGTTCAT | 1800 |
| GATAGCGATT | TGCGCCTTAT | AGATATCGGC | GCTGTACGCT | TTGGCCAGCT | 1850 |
| CACTCATATG | GCGATCCAGG | AACTCTCCAT | AGAATTTTCG | GCTGGCCAGC | 1900 |
| AACTGACTCT | GGTACATCGA | CTCTGACTTC | TGAGGAAAGT | CTGAAGCCGT | 1950 |
| ATAAAGATTG | GCCGGGCGAT | CCTCAATGAC | CTTTAGCGAT | TTTGCTTTGG | 2000 |
| CATCCATGAG | TGCATCAACG | ATACTCTTTT | CATCGCGGAT | GTCATTGGCA | 2050 |
| CTGACCGCTT | TACCTGGCAA | CCCCGCTTCA | CTCTTGAGTT | CATCAACCTC | 2100 |
| CTTCAGGGTT | TCATTTTTCAT | GGTTTTTCTT | GAGTTCTGAA | TGGGACTTAT | 2150 |
| CAAGCGTACT | TCTTAGCTTC | CTGTACTCCT | GCATTCCAGT | ACCGACATAC | 2200 |
| GGACTTGGTC | CTGGTGGGAC | AAATGGTGGA | GTACCGTAGC | TTGATCGAGC | 2250 |
| AGGAATATAC | TGGATTATGT | CACGCCCACC | ACCCTGCACA | TGTGTAATAA | 2300 |
| CCATCGAACC | AGGTTCTGTA | TCATTGACAG | CCATAGATCG | CCCCTACATT | 2350 |
| AATTTGAAAG | TGTAATGTAT | TGAGCGACTC | CCACCTAGAG | AACCCTCTCC | 2400 |
| CAGTCAATAA | GCCCCAATGC | ATCGGCAATA | CACTGCAATC | AACCTCAATA | 2450 |
| TCCCGTGTTT | AGATGATCCA | GAAGGTGCGC | TCTCTCGCCT | CTTATAATCG | 2500 |
| CGCCTGCGTC | AAACGGTCAT | TTCCTTAACG | CACACCTCAT | CTACCCCGGC | 2550 |
| CAGTCACGGA | AGCCGCATAC | CTTCGGTTCA | TTAACGAACT | CCCCTTTTCA | 2600 |
| AAATTCATCC | ATGCCGCCCC | TTCGCGAGCT | TCCGGACAAA | GCCACGCTGA | 2650 |
| TTGCGAGCCC | AGCGTTTTTG | ATTGCAAGCC | GCTGCAGCTG | GTCAGGCCGT | 2700 |
| TTCCGCAACG | CTTGAAGTCC | TGGCCGATAT | ACCGGCAGGG | CCAGCCATCG | 2750 |
| TTGACGAAT | AAAGCCACCT | CAGCCATGAT | GCCCTTTCCA | TCCCCAGCGG | 2800 |
| AACCCCGACA | TGGACGCCAA | AGCCCTGCTC | CTCGGCAGCC | TCTGCCTGGC | 2850 |
| CGCCCCATTC | GCCGACGCGG | CGACGCTCGA | CAATGCTCTC | TCCGCTGCC | 2900 |
| TCGCCGCCCG | GCTCGGTGCA | CCGCACACGG | CGGAGGGCCA | GTTGCACCTG | 2950 |
| CCACTCACCC | TTGAGGCCCG | GCGCTCCACC | GGCGAATGCG | GCTGTACCTC | 3000 |
| GGCGCTGGTG | CGATATCGGC | TGCTGGCCAG | GGGCGCCAGC | GCCGACAGCC | 3050 |
| TCGTGCTTCA | AGAGGGCTGC | TCGATAGTCG | CCAGGACACG | CCGCGCACGC | 3100 |
| TGACCCTGGC | GGCGGACGCC | GGCTTGCGCA | GCGGCCGCGA | ACTGGTCGTC | 3150 |

SUBSTITUTE SHEET

75

| | | | | | |
|------------|------------|------------|------------|-------------|------|
| ACCCTGGGTT | GTCAGGCGCC | TGACTGACAG | GCCGGGCTGC | CACCACCAGG | 3200 |
| CCGAGATGGA | CGCCCTGCAT | GTATCCTCCG | ATCGGCAAGC | CTCCCGTTTCG | 3250 |
| CACATTACAC | ACTCTGCAAT | CCAGTTCATA | AATCCCATAA | AAGCCCTCTT | 3300 |
| CCGCTCCCCG | CCAGCCTCCC | CGCATCCCCG | ACCCTAGACG | CCCCGCCGCT | 3350 |
| CTCCGCCGGC | TCGCCCCACA | AGAAAAACCA | ACCGCTCGAT | CAGCCTCATC | 3400 |
| CTTCACCCAT | CACAGGAGCC | ATCGCGATGC | ACCTGATACC | CCATTGGATC | 3450 |
| C | | | | | 3451 |

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

| | | | | | |
|------------|------------|-------------|------------|------------|-----|
| GGGTTCAGCA | AGCGTTCAGG | GGCGGTTTCAG | TACCCTGTCC | GTACTCTGCA | 50 |
| AGCCGTGAAC | GACACGACTC | TCGCAGAACG | GAGAAACACC | ATGAAAGCAC | 100 |
| TCAAGACTCT | CTTCATCGCC | ACCGCCCTGC | TGGGTTCGCG | CGCCGGCGTC | 150 |
| CAGGCCGCCG | ACAACTTCGT | CGGCCTGACC | TGGGGCGAGA | CCAGCAACAA | 200 |
| CATCCAGAAA | TCCAAGTCGC | TGAACCGCAA | CCTGAACAGC | CCGAACCTCG | 250 |
| ACAAGGTGAT | CGACAACACC | GGCACCTGGG | GCATCCGCGC | CGGCCAGCAG | 300 |
| TTCGAGCAGG | GCCGCTACTA | CGCGACCTAC | GAGAACATCT | CCGACACCAG | 350 |
| CAGCGGCAAC | AAGCTGCGCC | AGCAGAACCT | GCTCGGCAGC | TACGACGCCT | 400 |
| TCCTGCCGAT | CGGCGACAAC | AACACCAAGC | TGTTCGGCGG | TGCCACCCTC | 450 |
| GGCCTGGTCA | AGCTGGAACA | GGACGGCAAG | GGCTTCAAGC | GCGACAGCGA | 500 |
| TGTCGGCTAC | GCTGCCGGGC | TGCAGGCCGG | TATCCTGCAG | GAGCTGAGCA | 550 |
| AGAATGCCTC | GATCGAAGGC | GGCTATCGTT | ACCTGCGCAC | CAACGCCAGC | 600 |
| ACCGAGATGA | CCCCGCATGG | CGGCAACAAG | CTGGGCTCCC | TGGACCTGCA | 650 |
| CAGCAGCTCG | CAATTCTACC | TGGGCGCCAA | CTACAAGTTC | TAAATGACCG | 700 |
| CGCAGCGCCC | GCGAGGGCAT | GCTTCGATGG | CCGGGCCGGA | AGGT | 744 |

SUBSTITUTE SHEET

76

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2760 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

| | | | | | |
|-------------|-------------|------------|------------|-------------|------|
| CTGCAGCTGG | TCAGGCCGTT | TCCGCAACGC | TTGAAGTCCT | GGCCGATATA | 50 |
| CCGGCAGGGC | CAGCCATCGT | TCGACGAATA | AAGCCACCTC | AGCCATGATG | 100 |
| CCCTTTCCAT | CCCCAGCGGA | ACCCCGACAT | GGACGCCAAA | GCCCTGCTCC | 150 |
| TCGGCAGCCT | CTGCCTGGCC | GCCCCATTCG | CCGACGCGGC | GACGCTCGAC | 200 |
| AATGCTCTCT | CCGCCTGCCT | CGCCGCCCGG | CTCGGTGCAC | CGCACACGGC | 250 |
| GGAGGGCCAG | TTGCACCTGC | CACTCACCTT | TGAGGCCCGG | CGCTCCACCG | 300 |
| GCGAATGCGG | CTGTACCTCG | GCGCTGGTGC | GATATCGGCT | GCTGGCCAGG | 350 |
| GGCGCCAGCG | CCGACAGCCT | CGTGCTTCAA | GAGGGCTGCT | CGATAGTCGC | 400 |
| CAGGACACGC | CGCGCACGCT | GACCCTGGCG | GCGGACGCCG | GCTTGGCGAG | 450 |
| CGGCCCGGAA | CTGGTCGTCA | CCCTGGGTTG | TCAGGCGCCT | GA CTGACAGG | 500 |
| CCGGGCTGCC | ACCACCAGGC | CGAGATGGAC | GCCCTGCATG | TATCCTCCGA | 550 |
| TCGGCAAGCC | TCCCGTTCGC | ACATTACCA | CTCTGCAATC | CAGTTCATAA | 600 |
| ATCCCATAAA | AGCCCTCTTC | CGCTCCCCGC | CAGCCTCCCC | GCATCCCGCA | 650 |
| CCCTAGACGC | CCCGCCGCTC | TCCGCCGGCT | CGCCCGACAA | GAAAAACCAA | 700 |
| CCGCTCGATC | AGCCTCATCC | TTCACCCATC | ACAGGAGCCA | TCGCGATGCA | 750 |
| CCTGATACCC | CATTGGATCC | CCCTGGTCGC | CAGCCTCGGC | CTGCTCGCCG | 800 |
| GCGGCTCGTC | CGCGTCCGCC | GCCGAGGAAG | CCTTCGACCT | CTGGAACGAA | 850 |
| TGCGCCAAAG | CCTGCGTGCT | CGACCTCAAG | GACGGCGTGC | GTTCCAGCCG | 900 |
| CATGAGCGTC | GACCCGGCCA | TCGCCGACAC | CAACGGCCAG | GGCGTGCTGC | 950 |
| ACTACTCCAT | GGTCCTGGAG | GGCGGCAACG | ACGCGCTCAA | GCTGGCCATC | 1000 |
| GACAACGCCC | TCAGCATCAC | CAGCGACGGC | CTGACCATCC | GCCTCGAAGG | 1050 |
| CGGCGTCGAG | CCGAACAAGC | CGGTGCGCTA | CAGCTACACG | CGCCAGGCGC | 1100 |
| GCGGCAGTTG | GTCGCTGAAC | TGGCTGGTAC | CGATCGGCCA | CGAGAAGCCC | 1150 |
| TCGAACATCA | AGGTGTTTCAT | CCACGAACTG | AACGCCGGCA | ACCAGCTCAG | 1200 |
| CCACATGTCTG | CCGATCTACA | CCATCGAGAT | GGGCGACGAG | TTGCTGGCGA | 1250 |
| AGCTGGCGCG | CGATGCCACC | TTCTTCGTCA | GGGCGCACGA | GAGCAACGAG | 1300 |

SUBSTITUTE SHEET

77

| | | | | | |
|------------|------------|------------|------------|------------|------|
| ATGCAGCCGA | CGCTCGCCAT | CAGCCATGCC | GGGGTCAGCG | TGGTCATGGC | 1350 |
| CCAGACCCAG | CCGCGCCGGG | AAAAGCGCTG | GAGCGAATGG | GCCAGCGGCA | 1400 |
| AGGTGTTGTG | CCTGCTCGAC | CCGCTGGACG | GGGTCTACAA | CTACCTCGCC | 1450 |
| CAGCAACGCT | GCAACCTCGA | CGATACCTGG | GAAGGCAAGA | TCTACCGGGT | 1500 |
| GCTCGCCGGC | AACCCGGCGA | AGCATGACCT | GGACATCAAA | CCCACGGTCA | 1550 |
| TCAGTCATCG | CCTGCACTTT | CCCGAGGGCG | GCAGCCTGGC | CGCGCTGACC | 1600 |
| GCGCACCAGG | CTTGCCACCT | GCCGCTGGAG | ACTTTCACCC | GTCATCGCCA | 1650 |
| GCCGCGCGGC | TGGGAACAAC | TGGAGCAGTG | CGGCTATCCG | GTGCAGCGGC | 1700 |
| TGGTCGCCCT | CTACCTGGCG | GCGCGGCTGT | CGTGGAACCA | GGTCGACCAG | 1750 |
| GTGATCCGCA | ACGCCCTGGC | CAGCCCCGGC | AGCGGCGGCG | ACCTGGGCGA | 1800 |
| AGCGATCCGC | GAGCAGCCGG | AGCAGGCCCC | TCTGGCCCTG | ACCCTGGCCG | 1850 |
| CCGCCGAGAG | CGAGCGCTTC | GTCCGGCAGG | GCACCGGCAA | CGACGAGGCC | 1900 |
| GGCGCGGCCA | ACGCCGACGT | GGTGAGCCTG | ACCTGCCCCG | TCGCCGCCGG | 1950 |
| TGAATGCGCG | GGCCCCGGCG | ACAGCGGCGA | CGCCCTGCTG | GAGCGCAACT | 2000 |
| ATCCCACTGG | CGCGGAGTTC | CTCGGCGACG | GCGGCGACGT | CAGCTTCAGC | 2050 |
| ACCCGCGGCA | CGCAGAACTG | GACGGTGGAG | CGGCTGCTCC | AGGCGCACCG | 2100 |
| CCAAGTGGAG | GAGCGCGGCT | ATGTGTTCGT | CGGCTACCAC | GGCACCTTCC | 2150 |
| TCGAAGCGGC | GCAAAGCATC | GTCTTCGGCG | GGGTGCGCGC | GCGCAGCCAG | 2200 |
| GACCTCGACG | CGATCTGGCG | CGGTTTCTAT | ATCGCCGGCG | ATCCGGCGCT | 2250 |
| GGCCTACGGC | TACGCCCAGG | ACCAGGAACC | CGACGCACGC | GGCCGGATCC | 2300 |
| GCAACGGTGC | CCTGCTGCGG | GTCTATGTGC | CGCGCTCGAG | CCTGCCGGGC | 2350 |
| TTCTACCGCA | CCAGCCTGAC | CCTGGCCGCG | CCGGAGGCGG | CGGGCGAGGT | 2400 |
| CGAACGGCTG | ATCGGCCATC | CGCTGCCGCT | GCGCCTGGAC | GCCATCACCG | 2450 |
| GCCCCGAGGA | GGAAGGCGGG | CGCCTGGAGA | CCATTCTCGG | CTGGCCGCTG | 2500 |
| GCCGAGCGCA | CCGTGGTGAT | TCCCTCGGCG | ATCCCCACCG | ACCCGCGCAA | 2550 |
| CGTCGGCGGC | GACCTCGACC | CGTCCAGCAT | CCCCGACAAG | GAACAGGCGA | 2600 |
| TCAGCGCCCT | GCCGGACTAC | GCCAGCCAGC | CCGGCAAACC | GCCGCGCGAG | 2650 |
| GACCTGAAGT | AACTGCCGCG | ACCGGCCGGC | TCCCTTCGCA | GGAGCCGGCC | 2700 |
| TTCTCGGGGC | CTGGCCATAC | ATCAGGTTTT | CCTGATGCCA | GCCCAATCGA | 2750 |
| ATATGAATTC | | | | | 2760 |

SUBSTITUTE SHEET

78

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

| | | | | | |
|-------------|------------|------------|------------|------------|-----|
| TTGATGAAAT | GCATCGATTA | ATAAATTTTC | ATGTACGATT | AAAACGTTTT | 50 |
| TACCCTTACC | TTTTCGTACT | ACCTCTGCCT | GAAGTTGACC | ACCTTTAAAG | 100 |
| TGATTTCGTTG | AAATCCATTA | TGCTCATTAT | TAATACGATC | TATAAAAACA | 150 |
| AATGGAATGT | GATGATCGAT | GA | | | 172 |

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| GTTCCATTGA | CTCTGTATCA | CCTGTTGTAA | CGAACATCCA | TATGTCCTGA | 50 |
| AACTCCAACC | ACAGGTTTGA | CCACTTCCAA | TTTCAGACCA | CCAAGTTTGA | 100 |
| CACGTGAAGA | TTCATCTTCT | AATATTTCCG | AATTAATATC | ATATTATTTA | 150 |
| AATAG | | | | | 155 |

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET

79

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ACATAGAAAA | ACTCAAAAGA | TTTACTTTTT | TCAAATGGAA | AATAAGGGTA | 50 |
| CACACGATAT | TTCCCGTCAT | CTTCAGTTAC | CGGTACAACA | TCCTCTTTAT | 100 |
| TAACCTGCAC | ATAATCTGAC | TCCGCTTCAC | TCATCAAAC | ACTAA | 145 |

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTCACTGGA | ATTACATTT | GCTCATTAC | G | TACAGTGACA | ATCGCGTCAG | 50 |
| ATAGTTTCTT | CTGGTTAGCT | TGACTCTTAA | CAATCTTGTC | TAAATTTTGT | | 100 |
| TTAATTCCTT | GATTCGTA | AGAAATTTTA | CTTCTAATTC | CTTGTAATTC | | 150 |
| ATAACTTGCA | TTATCATATA | AATCATAAGT | ATCACATTTT | TGATGAATAC | | 200 |
| TTTGATATAA | ATCTGACAAT | ACAGGCAGTT | GCTCCATTCT | ATCGTTAAGA | | 250 |
| ATAGGGTAAT | TAATAG | | | | | 266 |

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

SUBSTITUTE SHEET

80

| | | | | | |
|--------------|------------|-------------|------------|-------------|-----|
| TGTTAAATTT | CTTTAACAGG | GATTTTGTTA | TTTAAATTAA | ACCTATTATT | 50 |
| TTGTGCGCTT | TTTCACTGCA | TCTACTGCTT | GAGTTGCTTT | TTCTGAAACC | 100 |
| GCCTCTTTCA | TTTCACTTGC | TTTTTCTGAT | GCTGCTTCTT | TCATTTTCGCC | 150 |
| TACTTTTTTCT | GACGCTGCTT | CTGTTGCTGA | TTTAATTACT | TCTTTTCGCAT | 200 |
| CTTCCACTTT | CTCTGCTACT | TTATTTTTTCA | CGTCTGTAGA | AAGCTGCTGT | 250 |
| GCTTTTTTCCT | TTACTTCAGT | CATTGTATTA | GCTGCAGCAT | CTTTTGTTC | 300 |
| TGATGCGACT | GATGCTACAG | TTTGCTTCGT | ATCCTCAACT | TTTTGTTTTG | 350 |
| CTTCTTGCTT | ATCAAAACAA | CCTGTCACGA | CTAAAGCTGA | ACCTAAAACC | 400 |
| AATGCTAATG | TTAATTTTTT | CATTATTTTC | TCCATAGAAT | AATTTGATTG | 450 |
| TTACAAAGCC | CTATTACTTT | GATGCAGTTT | AGTTTACGGG | AATTTTCATA | 500 |
| AAAAGAAAAA | CAGTAATAGT | AAAACTTTAC | CTTTCTTTAA | AAAGATTACT | 550 |
| TTATAAAAAA | ACATCTAAGA | TATTGATTTT | TAATAGATTA | TAAAAAACCA | 600 |
| ATAAAAAATTTT | ATTTTGTG | AAAAAAAAG | AATAGTTTAT | TTTAAATAAA | 650 |
| TTACAGGAGA | TGCTTGATGC | ATCAATATTT | CTGATTTATT | ACCATCCCAT | 700 |
| AATAATTGAG | CAATAGTTGC | AGGATAAAAT | GATATTGGAT | TTCGTTTTCC | 750 |
| ATACAGTTCA | GCAACAATTT | CTCCCACTAA | GGGCAAATGG | GAAACAATTA | 800 |
| ATACAGATTT | AACGCCCTCG | TCTTTTAGCA | CTTCTAAATA | ATCAA | 845 |

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

| | | | | | |
|------------|------------|------------|------------|-------------|-----|
| GAATAGAGTT | GCACTCAATA | GATTCGGGCT | TTATAATTGC | CCAGATTTTTT | 50 |
| ATTTATAACA | AAGGGTTCCT | AATGAAAAAA | TTTAATCAAT | CTCTATTAGC | 100 |
| AACTGCAATG | TTGTTGGCTG | CAGGTGGTGC | AAATGCGGCA | GCGTTTCAAT | 150 |
| TGGCGGAAGT | TTCTACTTCA | GGTCTTGGTC | GTGCCTATGC | GGGTGAAGCG | 200 |
| GCGATTGCAG | ATAATGCTTC | TGTCGTGGCA | ACTAACCCAG | CTTTGATGAG | 250 |
| TTTATTTAAA | ACGGCACAGT | TTTCCACAGG | TGGCGTTTAT | ATTGATTCTA | 300 |
| GAATTAATAT | GAATGGTGAT | GTAACCTCTT | ATGCTCAGAT | AATAACAAAT | 350 |
| CAGATTGGAA | TGAAAGCAAT | AAAGGACGGC | TCAGCTTCAC | AGCGTAATGT | 400 |
| TGTTCCCGGT | GCTTTTGTGC | CAAATCTTTA | TTTCGTTGCG | CCAGTGAATG | 450 |

INSTITUTE SHEET

81

| | | | | | |
|------------|------------|-------------|------------|------------|------|
| ATAAATTCGC | GCTGGGTGCT | GGAATGAATG | TCAATTTCCG | TCTAAAAAGT | 500 |
| GAATATGACG | ATAGTTATGA | TGCTGGTGTA | TTTGGTGGAA | AAACTGACTT | 550 |
| GAGTGCTATC | AACTTAAATT | TAAGTGGTGC | TTATCGAGTA | ACAGAAGGTT | 600 |
| TGAGCCTAGG | TTTAGGGGTA | AATGCGGTTT | ATGCTAAAGC | CCAAGTTGAA | 650 |
| CGGAATGCTG | GTCTTATTGC | GGATAGTGTT | AAGGATAACC | AAATAACAAG | 700 |
| CGCACTCTCA | ACACAGCAAG | AACCATTTCAG | AGATCTTAAG | AAGTATTTGC | 750 |
| CCTCTAAGGA | CAAATCTGTT | GTGTCATTAC | AAGATAGAGC | CGCTTGGGGC | 800 |
| TTTGGCTGGA | ATGCAGGTGT | AATGTATCAA | TTTAATGAAG | CTAACAGAAT | 850 |
| TGGTTTAGCC | TATCATTCTA | AAGTGGACAT | TGATTTTGCT | GACCGCACTG | 900 |
| CTACTAGTTT | AGAAGCAAAT | GTCATCAAAG | AAGGTAAAAA | AGGTAATTTA | 950 |
| ACCTTTACAT | TGCCAGATTA | CTTAGAACTT | TCTGGTTTCC | ATCAATTAAC | 1000 |
| TGACAAACTT | GCAGTGCATT | ATAGTTATAA | ATATACCCAT | TGGAGTCGTT | 1050 |
| TAACAAAATT | ACATGCCAGC | TTCGAAGATG | GTAAAAAAGC | TTTTGATAAA | 1100 |
| GAATTACAAT | ACAGTAATAA | CTCTCGTGTT | GCATTAGGGG | CAAGTTATAA | 1150 |
| TCTTTATGAA | AAATTGACCT | TACGTGCGGG | TATTGCTTAC | GATCAAGCGG | 1200 |
| CATCTCGTCA | TCACCGTAGT | GCTGCAATTC | CAGATACCGA | TCGCACTTGG | 1250 |
| TATAGTTTAG | GTGCAACCTA | TAAATTCACG | CCGAATTTAT | CTGTTGATCT | 1300 |
| TGGCTATGCT | TACTTAAAAG | GCAAAAAAGT | TCACTTTAAA | GAAGTAAAAA | 1350 |
| CAATAGGTGA | CAAACGTACA | TTGACATTGA | ATACAACGTC | AAATTATACT | 1400 |
| TCTCAAGCAC | ACGCAAATCT | TTACGGTTTG | AATTTAAATT | ATAGTTTCTA | 1450 |
| ATCCGTTAAA | AAATTTAGCA | TAATAAAGCA | CAATTCCACA | CTAAGTGTGC | 1500 |
| TTTTCTTTTA | TAAAACAAGG | CGAAAAATGA | CCGCACTTTA | TTACACTTAT | 1550 |
| TACCCCTCGC | CAGTCGGACG | GCTTTTGATT | TTATCTGACG | GCGAAACA | 1598 |

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9100 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| GTCAAAAATT | GCGTGCATTC | TAGCGAAAAA | ATGGGCTTTT | GGGAACTGTG | 50 |
| GGATTTATTT | AAAATCTTAG | AAAATCTTAC | CGCACTTTTA | AGCTATAAAG | 100 |
| TGCGGTGAAA | TTTAGTGGCG | TTTATAATGG | AGAATTACTC | TGGTGTAATC | 150 |

SUBSTITUTE SHEET

82

| | | | | | |
|------------|-------------|------------|-------------|-------------|------|
| CATTCGACTG | TCCAGCTTCC | AGTACCTTCT | GGAAC TAATG | TTTTTGTGAG | 200 |
| ATAAGGCAAA | ATTTCTTTCA | TTTGGGTTTC | TAATGTCCAA | GGTGGATTAA | 250 |
| TTACCACCAT | ACCGCTCGCA | GTCATTCTCT | GTTGATCGCT | ATCTGGGCGA | 300 |
| ACGGCGAGTT | CAATTTT TAG | AATTTTCTA | ATTCCC GTT | CTTCTAAACC | 350 |
| CTTAAAAATA | CGTTTAGTTT | GTTGGCGTAA | TACAACAGGA | TACCAAATCG | 400 |
| CATAAGTGCC | AGTGGCAAAA | CGTTTATAGC | CCTCTTCAAT | GGCTTTAACA | 450 |
| ACGAGATCAT | AATCATCTTT | TAATTCATAA | GGCGGATCGA | TGAGTACTAA | 500 |
| GCCTCGGCGT | TCTTTTGGCG | GAAGCGTTGC | TTTGACTTGT | TGAAAGCCAT | 550 |
| TGTCACATTT | TACGGTGACA | TTTTTGTCGT | CGCTAAAATT | ATTGCGAAGA | 600 |
| ATTGGATAAT | CGCTAGGATG | AAGCTCGGTC | AATAGTGCGC | GATCTTGTGA | 650 |
| GCGCAACAAT | TCCGCGGCAA | TTAATGGAGA | ACCCGCGTAA | TAACGTAGTT | 700 |
| CTTTGCCACC | ATAATTGAGT | TTTTTGATCA | TTTTTACATA | ACGAGCAATA | 750 |
| TCTTCGGGTA | AATCTGTTTG | ATCCCACAGG | CGTCCAATAC | CTTCTTTATA | 800 |
| TTCCCCCGTT | TTTTCTGATT | CATTTGAGGA | TAAACGATAA | CGCCCCACAC | 850 |
| CAGAGTGCGT | ATCCAAATAA | AAAAAGCCTT | TTTCTTTGAG | TTTAAGATTT | 900 |
| TCCAAAATGA | GCATTAAAAC | AATATGTTTC | AAGACATCGG | CATGATTGCC | 950 |
| AGCGTGAAAT | GAGTGATGAT | AACTCAGCAT | AATATATTCC | TTATATATTTC | 1000 |
| CTTATTTGTT | TAATAACGAA | GGCGAGCCAA | TTGACTCGCC | CGATTACACA | 1050 |
| CTAAAGTGCG | GTCATTTTFA | GAAGAGTTCT | TGTGGTTGCG | TCGCTGGCGT | 1100 |
| ATTGCCTTCA | TTATTTAAGC | GTTGCTGTAA | CTCAGTAGGA | ACATAATAAC | 1150 |
| CACGCTCTTG | CATTTCCGAA | AGATAGGTAC | GTGTCGGTTC | TGTTCCCGCA | 1200 |
| ATAAAATATT | CTTTGCGCCC | ACCGTTTGGA | GAAAGCAAAC | CTGTCAAAGT | 1250 |
| ATCAATGTTT | TTTTCCACAA | TTTTTGCGCG | TAGCGACAAT | TTACGTTCTG | 1300 |
| GCTTATCACT | CAAAGCCGTT | TTCATATAAG | TGATCCAAGC | AGGCATTGCT | 1350 |
| GTTTTTGCTC | CTGCTTCTCC | ACGCCCAAGT | ACTCGTTTGT | TATCATCAAA | 1400 |
| CCCGACATAA | GTTGTGGTTA | CTAAGTTTGC | ACCAAATCCC | GCATACCAAG | 1450 |
| CCACTTTTGA | ACTGTTGGTA | GTACCTGTTT | TACCGCCTAT | ATCGCTACGT | 1500 |
| TTAATGCTTT | GTGCAATACG | CCAGCTGGTG | CCTTTCCAGT | CTAAACCTTG | 1550 |
| TTCGCCATAA | ATTGCCGTAT | TTAAGGCACT | ACGAATGAGA | AAAGCAAGTT | 1600 |
| CGCCACTAAT | GACACGTGGC | GCATATTCTA | TTTTCGACGA | AGCATTTTTT | 1650 |
| GCAGCAGCCA | TTAAATCAAT | CGCATCTTCT | TTAAGTGCGG | TCATATTTGA | 1700 |
| TTGTAATTCT | GGCAGTTCAG | GCACAGTTTC | AGGTTGTTGA | TCTAATTCTT | 1750 |
| CGCCATTGGT | GCTGTCATCT | GTTGGTTTTA | AGGCATTCTC | GCCTAAAGGA | 1800 |
| ATATTGGCAA | AGCCGTTGAT | TTTGTCTTTG | GTTTCGCCAT | AAATTACAGG | 1850 |
| TATATCATTA | CATTCAATGC | AAGCAATTTT | AGGGTTTGCA | ATAAATAAGT | 1900 |
| CTTTACCCGT | GTTATCTTGA | ATTTTTTCAA | TGATATAAGG | TTCAATGAGG | 1950 |
| AAGCCACCAT | TATCAAACAC | CGCATAAGCT | CGCGCCATTT | CTAATGGTGT | 2000 |

SUBSTITUTE SHEET

83

| | | | | | |
|-------------|-------------|------------|-------------|-------------|------|
| GAAAGAGGCT | GCGCCAAGTG | CTAAGGCTTC | ACTGGCAAAA | TATTGATCAC | 2050 |
| GTTTAAAACC | AAAACGTTGT | AAAAATTCTG | CTGTGAAATC | AATACCTGCC | 2100 |
| GTTTGGATAG | CACGAATAGC | AATTATATTT | TTGGATTGAC | CTAATCCTAC | 2150 |
| GCGTAAACGC | ATCGGGCCAT | CATAACGATC | AGGCGAGTTT | TTCGGTTGCC | 2200 |
| ACATTTTTTTG | TCCCGGTTTT | TGAATAGAAA | TCGGGCTGTC | TTGTAATACG | 2250 |
| CTTGAAAGTG | TTAAGCCTTT | TTCTAATGCT | GCCGCGTAAA | TAAATGGTTT | 2300 |
| GATAGAAGAA | CCCACTTGAA | CTAAAGACTG | TGTGGCTCGA | TTGAATTTAC | 2350 |
| TTTGTTTCATA | GCTAAAGCCA | CCGACCACTG | CTTCAATCGC | ACCATTATCT | 2400 |
| GAATTAAGAG | AAACTAATGC | TGAATTTGCT | GCGGGAATTT | GTCTTAATTG | 2450 |
| CCATTCCCCA | TTAGCACGCT | GATGAATCCA | AATTTGCTCG | CCGACTTTCA | 2500 |
| CAGGATTGCT | TCTGCCTGTC | CAACGCATTG | CATTGGTTGA | TAAGGTCATT | 2550 |
| TTTTCCCCAG | AAGCGAGCAA | TATATCAGCA | CCGCCTTTTA | CAATTCCAAT | 2600 |
| CACTGCCGCA | GGAATAAATG | GCTCTGAATC | AGGTAGTTTG | CGTAGAAAAC | 2650 |
| CGACAATGCG | ATCATTGTCC | CAAGCGGCTT | CATTTTTTTG | CCATAATGGC | 2700 |
| GCGCCACCGC | GATAACCGTG | ACGCATATCG | TAATCAATCA | AGTTATTACG | 2750 |
| CACAGCTTTT | TGGGCTTCAG | CTTGGTCTTT | TGAAAGTACA | GTGGTAAATA | 2800 |
| CTTTATAACC | ACTGGTGTA | GCATTTTCTT | CGCCAAAACG | ACGCACCATT | 2850 |
| TCTTGACGCA | CCATTTTCAGT | GACATAATCG | GCTCGAAATT | CAAATTTTGC | 2900 |
| GCCGTGATAG | CTCGCCACAA | TCGGCTCTTT | CAATGCAGCA | TCATATTCTT | 2950 |
| CTTTGCTGAT | GTATTTTTCA | TCTAACATAC | GGCTTAGCAC | CACATTGCGG | 3000 |
| CGTTCTTCTG | AACGTTTTAA | AGAATAAAGC | GGGTTCATTG | TTGAAGGTGC | 3050 |
| TTTAGGTAAA | CCAGCAATAA | TCGCCATTTT | CGATAAGGTC | AATTCATTCA | 3100 |
| ATGATTTACC | GAAATAGGTT | TGTGCTGCCG | CTGCAACACC | ATAAGAACGA | 3150 |
| TAGCCTAAAA | AGATTTTGTT | TAAATAAAGC | TCTAATATTT | CTTGTTTGTT | 3200 |
| GAGAGTATTT | TCGATTTCTA | CCGCAAGCAC | GGCTTCACGA | GCTTTACGAA | 3250 |
| TAATGGTTTT | TTCTGAGGTT | AAGAAAAAGT | TACGCGCTAA | TTGTTGAGTA | 3300 |
| ATCGTACTTG | CGCCTTGTTA | TGCACCGCCA | TTACTCACTG | CGACAAACAA | 3350 |
| TGCACGGGCA | ATGCCGATAG | GGTCTAATCC | GTGATGATCG | TAAAAACGAC | 3400 |
| TGTCTTCCGT | CGCTAAAAAT | GCGTCAATTA | AGCGTTGTGG | CACATCGGCT | 3450 |
| AATTTCACTG | GAATACGGCG | TTGCTCACCC | ACTTCGCCAA | TTAATTTACC | 3500 |
| GTCAGCCGTA | TAAATCTGCA | TTGGTTGCTG | TAATTC AACG | GTTTTTAATG | 3550 |
| TTTCTACTGA | GGGCAATTCA | GATTTTAAGT | GGAAATACAA | CATTCCGCTT | 3600 |
| GCTACTAAAC | CTAAAATACA | TAAAGTTAAT | AGGGTGTTTA | ATATTAATTT | 3650 |
| TGCGATCCGC | ATCGTAAAT | TCTCGCTTCG | TTAATGAATA | TTCTTGTC AA | 3700 |
| GAGACCTATG | ATTTGGCTGT | TAAGTATAAA | AGATTCAGCC | TTTAAAGAAT | 3750 |
| AGGAAAGAAT | ATGCAATTCT | CCCTGAAAAA | TTACCGCACT | TTACAAATCG | 3800 |
| GCATTCATCG | TAAGCAGAGT | TATTTTGATT | TTGTGTGGTT | TGATGATCTC | 3850 |

SUBSTITUTE SHEET

84

| | | | | | |
|-------------|-------------|-------------|------------|-------------|------|
| GAACAGCCAC | AAAGTTATCA | AATCTTTGTT | AATGATCGTT | ATTTTAAAAA | 3900 |
| TCGTTTTTTA | CAACAGCTAA | AAACACAATA | TCAAGGGAAA | ACCTTTCCTT | 3950 |
| TGCAGTTTGT | AGCAAGCATT | CCCGCCCACT | TAACTTGGTC | GAAAGTATTA | 4000 |
| ATGTTGCCAC | AAGTGTTAAA | TGCGCAAGAA | TGTCATCAAC | AATGTAAATT | 4050 |
| TGTGATTGAA | AAAGAGCTGC | CTATTTTTTT | AGAAGAATTG | TGGTTTGATT | 4100 |
| ATCGTTCCTAC | CCCGTTAAAG | CAAGGTTTTT | GATTAGAGGT | TACTGCAATT | 4150 |
| CGTAAAAGTA | GCGCTCAAAC | TTATTTTGCA | GATTTTCAGC | CATTTAATAT | 4200 |
| TAATATATTG | GATGTTGCGT | CAAATGCTGT | TTTGCGTGCA | TTTCAATATC | 4250 |
| TGTTGAATGA | ACAAGTGCGG | TCAGAAAATA | CCTTATTTTT | ATTTCAAGAA | 4300 |
| GATGACTATT | GCTTGCGGAT | TTGTGAAAGA | TCTCAGCAAT | CACAAATTTT | 4350 |
| ACAATCTCAC | GAAAATTTGA | CCGCACTTTA | TGAACAATTT | ACCGAACGTT | 4400 |
| TTGAAGGACA | ACTTGAACAA | GTTTTTGTTT | ATCAAATTC | CTCAAGTCAT | 4450 |
| ACACCATTAC | CCGAAACTG | GCAGCGAGTA | GAAACAGAAC | TCCCTTTTAT | 4500 |
| TGCGCTGGGC | AACGCGCTAT | GGCAAAAAGA | TTTACATCAA | CAAAAAGTGG | 4550 |
| GTGGTTAAAT | GTCGATGAAT | TTATTGCCCT | GGCGTACTTA | TCAACATCAA | 4600 |
| AAGCGTTTAC | GTCGTTTAGC | TTTTTATATC | GCTTTATTTA | TCTTGCTTGC | 4650 |
| TATTAATTTA | ATGTTGGCTT | TTAGCAATTT | GATTGAACAA | CAGAAACAAA | 4700 |
| ATTTGCAGGC | ACAGCAAAAG | TCGTTTGAAC | AACTTAATCA | ACAGCTTCAT | 4750 |
| AAAACCTACCA | TGCAAATTGA | TCAGTTACGC | ATTGCGGTGA | AAAGTTGGTGA | 4800 |
| AGTTTTGACA | TCTATTCCCA | ACGAGCAAGT | AAAAAAGAGT | TTACAACAGC | 4850 |
| TAAGTGAATT | ACCTTTTCAA | CAAGGAGAAC | TGAATAAATT | TAAACAAGAT | 4900 |
| GCCAATAACT | TAAGCTTGGA | AGGTAACGCG | CAAGATCAAA | CAGAAATTTGA | 4950 |
| ACTGATTTCAT | CAATTTTTTAA | AGAAACATTT | TCCCAATGTG | AAATTAAGTC | 5000 |
| AGGTTCAACC | TGAACAAGAT | ACATTGTTTT | TTCACTTTGA | TGTGGAACAA | 5050 |
| GGGGCGGAAA | AATGAAAGCT | TTTTTTAACG | ATCCTTTTAC | TCCTTTTGGG | 5100 |
| AAATGGCTAA | GTCAGCCTTT | TTATGTGCAC | GGTTTAACCT | TTTTATTGCT | 5150 |
| ATTAAGTGCG | GTGATTTTTT | GCCCCGTTTT | AGATTATATA | GAGGGGAGTT | 5200 |
| CACGTTTCCA | TGAAATTGAA | AATGAGTTAG | CGGTGAAACG | TTCAGAATTG | 5250 |
| TTGCATCAAC | AGAAAATTTT | AACCTCTTTA | CAACAGCAGT | CGGAAAGTCG | 5300 |
| AAAACCTTCT | CCAGAACTGG | CTGCACAAAT | TATTCCTTTG | AATAAACAAA | 5350 |
| TTCAACGTTT | AGCTGCGCGT | AACGGTTTTAT | CTCAGCATTT | ACGTTGGGAA | 5400 |
| ATGGGGCAAA | AGCCTATTTT | GCATTTACAG | CTTACAGGTC | ATTTTGAAAA | 5450 |
| AACGAAGACA | TTTTTATCCG | CACTTTTGGC | TAATTCGTCA | CAGCTTTCTG | 5500 |
| TAAGTCGGTT | GCAATTTATG | AAACCCGAAG | ACGGCCCAT | GCAAACCGAG | 5550 |
| ATCATTTTTT | AGCTAGATAA | GGAAACAAAA | TGAAACATTG | GTTTTTCCTG | 5600 |
| ATTATATTAT | TTTTTATGAA | TTGCAGTTGG | GGACAAGATC | CTTTCGATAA | 5650 |
| AACACAGCGT | AACCGTTCTC | AGTTTGATAA | CGCACAAACA | GTAATGGAGC | 5700 |

SUBSTITUTE SHEET

85

| | | | | | |
|------------|------------|-------------|------------|-------------|------|
| AAACAGAAAT | AATTCCTCA | GATGTGCCTA | ATAATCTATG | CGGAGCGGAT | 5750 |
| GAAAATCGCC | AAGCGGCTGA | AATTCCTTTG | AACGCTTTAA | AATTGGTGGG | 5800 |
| GGTAGTGATT | TCTAAAGATA | AAGCCTTTGC | CTTGTTGCAA | GATCAAGGTT | 5850 |
| TGCAAGTTTA | CAGCGTTTTA | GAGGGCGTTG | ATGTGGCTCA | AGAGGGCTAT | 5900 |
| ATTGTAGAAA | AAATCAACCA | AAACAATGTT | CAATTTATGC | GTAAGCTAGG | 5950 |
| AGAGCAATGT | GATAGTAGTG | AATGGAAAAA | ATTAAGTTTT | TAAAGGAAGA | 6000 |
| TTATGAAGAA | ATATTTTTTA | AAGTGC GGTT | ATTTTTTAGT | ATGTTTTTGT | 6050 |
| TTGCCATTAA | TCGTTTTTGC | TAATCCTAAA | ACAGATAACG | AACGTTTTTT | 6100 |
| TATTCGTTTA | TCGCAAGCAC | CTTTAGCTCA | AACACTGGAG | CAATTAGCTT | 6150 |
| TTCAACAAGA | TGTGAATTTA | GTGATTGGAG | ATATATTGGA | AAACAAGATC | 6200 |
| TCTTTGAAAT | TAAACAATAT | TGATATGCCA | CGTTTGCTAC | AAATAATCGC | 6250 |
| AAAAAGTAAG | CATCTTACTT | TGAATAAAGA | TGATGGGATT | TATTATTTAA | 6300 |
| ACGGCAGTCA | ATCTGGCAAA | GGTCAGGTTG | CAGGAAATCT | TACGACAAAT | 6350 |
| GAACCGCACT | TAGTGAGTCA | CACGGTAAAA | CTCCATTTTG | CTAAAGCTTC | 6400 |
| TGAATTAATG | AAATCCTTAA | CAACAGGAAG | TGGCTCCTTG | CTTTCTCCCG | 6450 |
| CTGGGAGCAT | TACCTTTGAT | GATCGCAGTA | ATTTGCTGGT | TATTCAGGAT | 6500 |
| GAACCTCGTT | CTGTGCAAAA | TATCAAAAAA | CTGATTGCTG | AAATGGATAA | 6550 |
| GCCTATTGAA | CAGATCGCTA | TTGAAGCGCG | AATTGTGACA | ATTACGGATG | 6600 |
| AGAGTTTGAA | AGAACTTGGC | GTTCCGGTGGG | GGATTTTTTA | TCCAAC TGAA | 6650 |
| AATGCAAGAC | GAGTTGCGGG | CAGCCTTACA | GGCAATAGCT | TTGAAAATAT | 6700 |
| TGCGGATAAT | CTTAATGTAA | ATTTTGCGAC | AACGACGACA | CCTGCTGGCT | 6750 |
| CTATAGCATT | ACAAGTCGCC | AAAATTAATG | GGCGATTGCT | TGATTTAGAA | 6800 |
| TTGAGTGCGT | TGGAGCGTGA | AAATAATGTA | GAAATTATTG | CAAGCCCTCG | 6850 |
| CTTACTCACT | ACCAATAAGA | AAAGTGCGAG | CATTAAACAG | GGGACAGAAA | 6900 |
| TTCTTTACAT | CGTGAGTAAT | ACTCGTAACG | ATACGCAATC | TGTGGAATTT | 6950 |
| CGTGAGGCGG | TGCTTGGTTT | GGAAGTGACG | CCACATATTT | CTAAAGATAA | 7000 |
| CAATATCTTA | CTTGATTTAT | TGGTAAGTCA | AAATTCCCCT | GGTTCTCGTG | 7050 |
| TCGCTTATGG | ACAAAATGAG | GTGGTTTCTA | TTGATAAACA | AGAAATTAAT | 7100 |
| ACTCAGGTTT | TTGCCAAAGA | TGGGGAAACC | ATTGTGCTTG | GCGGCGTATT | 7150 |
| TCACGATACA | ATCACGAAAA | GCGAAGATAA | AGTGCCATTG | CTTGGCGATA | 7200 |
| TACCCGTTAT | TAAACGATTA | TTTAGCAAAG | AAAGTGAACG | ACATCAAAAA | 7250 |
| CGTGAGCTAG | TGATTTTCGT | CACGGCACAT | ATTTTAAAAG | CAGGAGAAAA | 7300 |
| CGTTAGAGGC | GTTGAAACAA | AAAAGTGAGG | GTAAAAAATA | ACTTTTTTAA | 7350 |
| TGATGAATTT | TTTTAATTTT | CGCTGTATCC | ACTGTCGTGG | CAATCTTCAT | 7400 |
| ATCGCAAAAA | ATGGGTTATG | TTCAGGTTGC | CAAAAACAAA | TTAAATCTTT | 7450 |
| TCCTTATTGC | GGTCATTGTG | GTTCCGAATT | GCAATATTAT | GCGCAGCATT | 7500 |
| GTGGGAATTG | TCTTAAACAA | GAACCAAGTT | GGGATAAGAT | GGTCATTATT | 7550 |

SUBSTITUTE SHEET

86

| | | | | | |
|------------|------------|------------|------------|------------|------|
| GGGCATTATA | TTGAACCTCT | TTCGATATTG | ATTCAGCGTT | TTAAATTTCA | 7600 |
| AAATCAATTT | TGGATTGACC | GCACTTTAGC | TCGGCTTTTA | TATCTTGCGG | 7650 |
| TACGTGATGC | TAAACGAACG | CATCAACTTA | AATTGCCAGA | GGCAATCATT | 7700 |
| CCAGTGCCTT | TATATCATTT | TCGTCACTGG | CGACGGGGTT | ATAATCAGGC | 7750 |
| AGATTTATTA | TCTCAGCAAT | TAAGTCGTTG | GCTGGATATT | CCTAATTTGA | 7800 |
| ACAATATCGT | AAAGCGTGTG | AAACACACCT | ATACTCAACG | TGGTTTGAGT | 7850 |
| GCAAAAGATC | GTCGTCAGAA | TTTAAAAAAT | GCCTTTTCTC | TTGCTGTTTC | 7900 |
| GAAAAATGAA | TTTCCTTATC | GTCGTGTTGC | GTTGGTGGAT | GATGTGATTA | 7950 |
| CTACTGGTTC | TACACTCAAT | GAAATCTCAA | AATTGTTGCG | AAAATTAGGT | 8000 |
| GTGGAGGAGA | TTCAAGTGTG | GGGGCTGGCA | CGAGCTTAAT | ATAAAGCACT | 8050 |
| GGAAAAAATA | GCGCGATAAG | CGTATTATTC | CCGATACTTT | CTCTCAAGTA | 8100 |
| TTTAGGACAT | AATTATGGAA | CAAGCAACCC | AGCAAATCGC | TATTTCTGAT | 8150 |
| GCCGCACAAG | CGCATTTTCG | AAAACCTTTA | GACACCCAAG | AAGAAGGAAC | 8200 |
| GCATATTCGT | ATTTTCGCGG | TTAATCCTGG | TACGCCTAAT | GCGGAATGTG | 8250 |
| GCGTATCTTA | TTGCCCCCCG | AATGCCGTGG | AAGAAAGCGA | TATTGAAATG | 8300 |
| AAATATAATA | CTTTTCTGTC | ATTTATTGAT | GAAGTGAGTT | TGCCTTTCTT | 8350 |
| AGAAGAAGCA | GAAATTGATT | ATGTTACCGA | AGAGCTTGGT | GCGCAACTGA | 8400 |
| CCTTAAAAGC | ACCGAATGCC | AAAATGCGTA | AGGTGGCTGA | TGATGCGCCA | 8450 |
| TTGATTGAAC | GTGTTGAATA | TGTAATTCAA | ACTCAAATTA | ACCCACAGCT | 8500 |
| TGCAAATCAC | GGTGGACGTA | TAACCTTAAT | TGAAATTACT | GAAGATGGTT | 8550 |
| ACGCAGTTTT | ACAATTTGGT | GGTGGCTGTA | ACGGTTGTTC | AATGGTGGAT | 8600 |
| GTTACGTTAA | AAGATGGGGT | AGAAAAACAA | CTTGTTAGCT | TATTCCTGAA | 8650 |
| TGAATTAAAA | GGTGCAAAAG | ATATAACTGA | GCATCAACGT | GGCGAACATT | 8700 |
| CTTATTATTA | GTGAGTTATA | AAAGAAGATT | TATAATGACC | GCACTTTTGA | 8750 |
| AAGTGCGGTT | ATTTTTATGG | AGAAAAAATG | AAAATACTTC | AACAAGATGA | 8800 |
| TTTTGGTTAT | TGGTTGCTTA | CACAAGGTTT | TAATCTGTAT | TTAGTGAATA | 8850 |
| ATGAATTGCC | TTTTGGTATC | GCTAAAGATA | TTGATTTGGA | AGGATTGCAG | 8900 |
| GCAATGCAAA | TTGGGGAATG | GAAAAATTAT | CCGTTGTGGC | TTGTGGCTGA | 8950 |
| GCAAGAAAGT | GATGAACGAG | AATATGTGAG | TTTGAGTAAC | TTGCTTTCAC | 9000 |
| TGCCAGAGGA | TGAATTCCAT | ATATTAAGCC | GAGGTGTGGA | AATTAATCAT | 9050 |
| TTTCTGAAAA | CCCATAAATT | CTGTGGAAAG | TGCGGTCATA | AAACACAACA | 9100 |

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET

87

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| AAAAATCGAC | TGCCGTCATT | TTCAACCACC | ACATAGCTCA | TATTCGCAAG | 50 |
| CCAATGTATT | GACCGTTGGG | AATAATAACA | GCCCCAAAAC | AATGAAACAT | 100 |
| ATGGTGATGA | GCCAAACATA | CTTTCCTGCA | GATTTTGGAA | TCATATCGCC | 150 |
| ATCAGCACCA | GTATGGTTTG | ACCAGTATTT | AACGCCATAG | ACATGTGTAA | 200 |
| AAAAATTAAA | TAACGGTGCA | AGCATGAGAC | CAACGGCACC | TGATGTACCT | 250 |
| TGTACGATGA | CCTCACCTGC | TGTGGCAACC | ATACCAAGTC | CATTGCCTGT | 300 |
| GATATTTTGT | CGAAAAGACA | AACTTACCAC | ACAGACCAAG | CCGATGATTG | 350 |
| AGATGACAAA | ATAAAACCAA | TCCAAATGCG | TGTGAGCTGT | TGTGGTCCAA | 400 |
| AATCCAGTAA | ATAGTGCAAT | AAATCCGCAA | ACAAACCAAA | GTAGCACCCA | 450 |
| GCTTGTGTGC | CAATCTTTTT | TACCAAAGCC | TGTGATGTTA | TCTAAAATAT | 500 |
| CAATTTTCAT | CAGATTTTCC | CTAAT | | | 525 |

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TAATGATAAC | CAGTCAAGCA | AGCTCAAATC | AGGGTCAGCC | TGTTTTGAGC | 50 |
| TTTTTATTTT | TTGATCATCA | TGCTTAAGAT | TCACTCTGCC | ATTTTTTTAC | 100 |
| AACCTGCACC | ACAAGTCATC | ATCGCATTTG | CAAAAATGGT | ACAAACAAGC | 150 |
| CGTCAGCGAC | TTAAACAAAA | AAAGGCTCAA | TCTGCGTGTG | TGCGTTCACT | 200 |
| TTTACAAATC | ACCATGCACC | GCTTTGACAT | TGTTGGTGAA | TTTCATGACC | 250 |
| ATGCACACCC | TTATTATATT | AACTCAAATA | AAATACGCTA | CTTTGTCAGC | 300 |
| TTTAGCCATT | CAGATAATCA | AGTCGCTCTC | ATCATCAGCT | TAACACCTTG | 350 |
| TGCCATTGAC | ATAGAAGTTA | ACGATATTAA | ATACAGTGTG | GTTGAACGAT | 400 |
| ACTTTCATCC | CAATGAAATT | TATCTACTTA | CTCAATTTAG | CTCTACTGAT | 450 |
| AGGCAACAGC | TTATTA | | | | 466 |

SUBSTITUTE SHEET

88

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

| | | | | | |
|------------|------------|------------|-------------|-------------|-----|
| GATCTTTGAT | TTTCATTGAG | TATTACTCTC | TCTTGTCACT | TCTTTCTATT | 50 |
| TTACCATAAA | GTCCAGCCTT | TGAAGAACTT | TTACTAGAAG | ACAAGGGGCT | 100 |
| TCTGTCTCTA | TTTGCCATCT | TAGGCATCAA | AAAAGAGGGG | TCATCCCTCT | 150 |
| TTACGAATTC | AATGCTACTA | GGGTATCCAA | ATACTGGTTG | TTGATGACTG | 200 |
| CCAAAATATA | GGTATCTGCT | TTCAAGAGGT | CATCTGGTCC | AAATTCAACA | 250 |
| TCCAATGGGG | AATTTTCCTG | CTCTCGGAAA | CCCAAAATAT | TCAGATTGTA | 300 |
| TTTGCCACGG | AGGTCTAATT | TACTTCAGAC | TTTGACCTGC | CCAAGACTGA | 350 |
| GGAATTTTCA | TCTCCACGAT | AGACACATTT | TTATCCAACT | GAAAGACATC | 400 |
| AACACTATTA | TGAAAAGAAT | GGTCTGTGCT | AGAGACTGCC | CCATTTTCATA | 450 |
| CTCTGGCGAG | ATAACCGAGT | CAGCTCCAAT | CTTTTCTAGC | ACTTTCTTAG | 500 |
| CGGTCTGACT | TTTGACCTTA | GCAATAACAG | TCGGTACCCC | CAAACCTCTTA | 550 |
| CAGTGCATAA | CCGCAAGCAC | ACTCGACTCC | AGATTTTTCAC | CTGTCGCGAC | 600 |
| TACAACGGTA | TCGCAGGTAT | CAATCCCTGC | T | | 631 |

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3754 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CCAATATTTT | GGTCAGCATA | GTGTTCTTTT | TCAGTGGTAA | CAGCTTGCAA | 50 |
| TACTTGAGCA | GAAATGGCAG | ATTTATCAAG | GAAAAAGTTA | ACGTAAGGTC | 100 |

SUBSTITUTE SHEET

89

| | | | | | |
|-------------|--------------|------------|-------------|-------------|------|
| CTGTTGCGAC | AAC TTTTTC A | AAGGCTTGGC | TGTTCA TTTT | TTCAGCCAGT | 150 |
| TCAGCCGCAA | TCATTTGTGG | TGCTTTACGT | TCGACTTTTG | CAAGAGAAAA | 200 |
| AGCAGGGAAA | GCAATGTCTC | CCATTTCTGA | GTTTTTAGGG | GTTTCCAGTA | 250 |
| ACTTTAAAAT | AGCCTCTTGG | TCCAGGCTAT | CAATGATGCT | AGATAATTCTG | 300 |
| CTAGCAATCA | ATTC TTTTGT | ATTCATTAAG | AGCTCCTTTT | TGGACTTTTC | 350 |
| TACTATTTTA | TCACAATTTT | AAAGAAAGAA | GAAAAAATTT | TTGAAATCTC | 400 |
| CTGTTTTTTT | GGTATAATAT | GGTTATAAAT | ATAGTTATAA | ATATAGTTAT | 450 |
| AAATATGCAC | GCAAGAGGAT | TTTATGAGAA | AAAGAGATCG | TCATCAGTTA | 500 |
| ATAAAAAAAA | TGATTACTGA | GGAGAAATTA | AGTACACAAA | AAGAAATTCA | 550 |
| AGATCGGTTG | GAGGCGCACA | ATGTTTGTGT | GACGCAGACA | ACCTTGCTCTC | 600 |
| GTGATTTGCG | CGAAATCGGC | TTGACCAAGG | TCAAGAAAAA | TGATATGGTG | 650 |
| TATTATGTAC | TAGTAAATGA | GACAGAAAAG | ATTGATTTGG | TGGAATTTTT | 700 |
| GTCTCATCAT | TTAGAAGGTG | TTGCAAGAGC | AGAGTTTACC | TTGGTGCTTC | 750 |
| ATACCAAATT | GGGAGAAGCC | TCTGTTTTGG | CAAATATTGT | AGATGTAAAC | 800 |
| AAGGATGAAT | GGATTTTAGG | AACAGTTGCT | GGTGCCAATA | CCTTATTGGT | 850 |
| TATTTGTCTGA | GATCAGCACG | TTGCCAAACT | CATGGAAGAT | CGTTTGCTAG | 900 |
| ATTTGATGAA | AGATAAGTAA | GGTCTTGGA | GTTGCTCTCA | AGACTTATTT | 950 |
| TTGAAAAGGA | GAGACAGAAA | ATGGCGATAG | AAAAGCTATC | ACCCGGCATG | 1000 |
| CAACAGTATG | TGGATATTAA | AAAGCAATAT | CCAGATGCTT | TTTTGCTCTT | 1050 |
| TCGGATGGGT | GATTTTTATG | AATTATTTTA | TGAGGATGCG | GTCAATGCTG | 1100 |
| CGCAGATTCT | GGAAATTTCC | TTAACGAGTC | GCAACAAGAA | TGCCGACAAT | 1150 |
| CCGATCCCTA | TGGCGGGTGT | TCCCTATCAT | TCTGCCCAAC | AGTATATCGA | 1200 |
| TGTCTTGATT | GAGCAGGGTT | ATAAGGTGGC | TATCGCAGAG | CAGATGGAAG | 1250 |
| ATCCTAAACA | AGCAGTTGGG | GTTGTTAAAC | GAGAGGTTGT | TCAGGTCATT | 1300 |
| ACGCCAGGGA | CAGTGGTCGA | TAGCAGTAAG | CCGGACAGTC | AGAATAATTT | 1350 |
| TTTGGTTTCC | ATAGACCGCG | AAGGCAATCA | ATTTGGCCTA | GCTTATATGG | 1400 |
| ATTTGGTGAC | GGGTGACTTT | TATGTGACAG | GTCTTTTGGA | TTTCACGCTG | 1450 |
| GTTTGTGGGG | AAATCCGTAA | CCTCAAGGCT | CGAGAAGTGG | TGTTGGGTTA | 1500 |
| TGACTTGTCT | GAGGAAGAAG | AACAAATCCT | CAGCCGCCAG | ATGAATCTGG | 1550 |
| TACTCTCTTA | TGAAAAAGAA | AGCTTTGAAG | ACCTTCATTT | ATTGGATTTG | 1600 |
| CGATTGGCAA | CGGTGGAGCA | AACGGCATCT | AGTAAGCTGC | TCCAGTATGT | 1650 |
| TCATCGGACT | CAGATGAGGG | AATTGAACCA | CCTCAAACCT | GTTATCCGCT | 1700 |
| ACGAAATTAA | GGATTTCTTG | CAGATGGATT | ATGCGACCAA | GGCTAGTCTG | 1750 |
| GATTTGGTTG | AGAATGCTCG | CTCAGGTAAG | AAACAAGGCA | GTCTTTTCTG | 1800 |
| GCTTTTGAT | GAAACCAAAA | CGGCTATGGG | GATGCGTCTC | TTGCGTTCTT | 1850 |
| GGATTCATCG | CCCCTTGATT | GATAAGGAAC | GAATCGTCCA | ACGTCAAGAA | 1900 |
| GTAGTGACAG | TCTTTCTCGA | CCATTTCTTT | GAGCGTAGTG | ACTTGACAGA | 1950 |

SUBSTITUTE SHEET

90

| | | | | | |
|------------|-------------|-------------|------------|-------------|------|
| CAGTCTCAAG | GGTGTTTATG | ACATTGAGCG | CTTGGCTAGT | CGTGTTTCTT | 2000 |
| TTGGCAAAAC | CAATCCAAAG | GATCTCTTGC | AGTTGGCGAC | TACCTTGTCT | 2050 |
| AGTGTGCCAC | GGATTTCGTGC | GATTTTAGAA | GGGATGGAGC | AACCTACTCT | 2100 |
| AGCCTATCTC | ATCGCACAAAC | TGGATGCAAT | CCCTGAGTTG | GAGAGTTTGA | 2150 |
| TTAGCGCAGC | GATTGCTCCT | GAAGCTCCTC | ATGTGATTAC | AGATGGGGGA | 2200 |
| ATTATCCGGA | CTGGATTTGA | TGAGACTTTA | GACAAGTATC | GTTGCGTTCT | 2250 |
| CAGAGAAGGG | ACTAGCTGGA | TTGCTGAGAT | TGAGGCTAAG | GAGCGAGAAA | 2300 |
| ACTCTGGTAT | CAGCACGCTC | AAGATTGACT | ACAATAAAAA | GGATGGCTAC | 2350 |
| TATTTTCATG | TGACCAATTC | GCAACTGGGA | AATGTGCCAG | CCCACTTTTT | 2400 |
| CCGCAAGGCG | ACGCTGAAAA | ACTCAGAACG | CTTTGGAACC | GAAGAATTAG | 2450 |
| CCCGTATCGA | GGGAGATATG | CTTGAGGCGC | GTGAGAAGTC | AGCCAACCTC | 2500 |
| GAATACGAAA | TATTTATGCG | CATTCGTGAA | GAGGTCGGCA | AGTACATCCA | 2550 |
| GCGTTTACAA | GCTCTAGCCC | AAGGAATTGC | GACGGTTGAT | GTCTTACAGA | 2600 |
| GTCTGGCGGT | TGTGGCTGAA | ACCCAGCATT | TGATTGACC | TGAGTTTGGT | 2650 |
| GACGATTCAC | AAATTGATAT | CCGGAAAGGG | CGCCATGCTG | TCGTTGAAAA | 2700 |
| GGTTATGGGG | GCTCAGACCT | ATATTCCAAA | TACGATTGAG | ATGGCAGAAG | 2750 |
| ATACCAGTAT | TCAATTGGTT | ACAGGGCCAA | ACATGAGTGG | GAAGTCTACC | 2800 |
| TATATGCGTC | AGTTAGCCAT | GACGGCGGTT | ATGGCCAGC | TGGGTTCCCTA | 2850 |
| TGTTCTTGCT | GAAAGCGCCC | ATTTACCGAT | TTTTGATGCG | ATTTTTACCC | 2900 |
| GTATCGGAGC | AGCAGATGAC | TTGGTTTCGG | GTCAGTCAAC | CTTTATGGTG | 2950 |
| GAGATGATGG | AGGCCAATAA | TGCCATTTTCG | CATGCGACCA | AGAACTCTCT | 3000 |
| CATTCTCTTT | GATGAATTGG | GACGTGGAAC | TGCAACTTAT | GACGGGATGG | 3050 |
| CTCTTGCTCA | GTCCATCATC | GAATATATCC | ATGAGCACAT | CGGAGCTAAG | 3100 |
| ACCCTCTTTG | CGACCCACTA | CCATGAGTTG | ACTAGTCTGG | AGTCTAGTTT | 3150 |
| ACAACACTTG | GTCAATGTCC | ACGTGGCAAC | TTTGAGCAG | GATGGGCAGG | 3200 |
| TCACCTTCCT | TCACAAGATT | GAACCGGGAC | CAGCTGATAA | ATCCTACGGT | 3250 |
| ATCCATGTTG | CCAAGATTGC | TGGCTTGCCA | GCAGACCTTT | TAGCAAGGGC | 3300 |
| GGATAAGATT | TTGACTCAGC | TAGAGAATCA | AGGAACAGAG | AGTCCTCCTC | 3350 |
| CCATGAGACA | AACTAGTGCT | GTCAGTGAAC | AGATTTCACT | CTTTGATAGG | 3400 |
| GCAGAAGAGC | ATCCTATCCT | AGCAGAATTA | GCTAAACTGG | ATGTGTATAA | 3450 |
| TATGACACCT | ATGCAGGTTA | TGAATGTCTT | AGTAGAGTTA | AAACAGAAAC | 3500 |
| TATAAAACCA | AGACTCACTA | GTTAATCTAG | CTGTATCAAG | GAGACTTCTT | 3550 |
| TGACAATTCT | CCACTTTTTT | GCTAGAATAA | CATCACACAA | ACAGAATGAA | 3600 |
| AAGGGCTGAC | GCATTGTCGC | TCCCTTTTGT | CTATTTTTTA | AGGAGAAAGT | 3650 |
| ATGCTGATTG | AGAAAATAAA | AACCTACAAG | TGGCAGGCCC | TGCTTCGCTC | 3700 |
| CTGATGACAG | GCTTGATGGT | TGCTAGTTCA | CTTCTGCAAC | CGCGTTATCT | 3750 |
| GCAG | | | | | 3754 |

SUBSTITUTE SHEET

91

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

| | | | | | |
|------------|------------|-------------|-------------|------------|------|
| AACAAAATAA | AAGAACTTAC | CTATTTTCCA | TCCAAAATGT | TTAGCAATCA | 50 |
| TCATCTGCAA | GGCAACGTAT | TGCATGGCAT | TGATGTGATG | AGCAACTAAT | 100 |
| ATGTCATTAG | AACGTTGCGT | CAAAC TAGCA | TCTAAATAAA | GATCGAAATG | 150 |
| CAGTTATCAA | AAATGCAAGC | TCCTATCGGC | CCTTGTTTTA | ATTATTACTC | 200 |
| ACATTGCCTT | AATGTATTTA | CTTGCTTATT | ATTAAC TTTT | TTGCTAAGTT | 250 |
| AGTAGCGTCA | GTTATTCATT | GAAAGGACAT | TATTATGAAA | ATTCTTGTA | 300 |
| CAGGCTTTGA | TCCCTTTGGC | GGCGAAGCTA | TTAATCCTGC | CCTTGAAGCT | 350 |
| ATCAAGAAAT | TGCCAGCAAC | CATTCATGGA | GCAGAAATCA | AATGTATTGA | 400 |
| AGTTCCAACG | GTTTTTCAAA | AATCTGCCGA | TGTGCTCCAG | CAGCATATCG | 450 |
| AAAGCTTTCA | ACCTGATGCA | GTCCTTTGTA | TTGGGCAAGC | TGGTGGCCGG | 500 |
| ACTGGACTAA | CGCCAGAACG | CGTTGCCATT | AATCAAGACG | ATGCTCGCAT | 550 |
| TCCTGATAAC | GAAGGGAATC | AGCCTATTGA | TACACCTATT | CGTGCAGATG | 600 |
| GTAAAGCAGC | TTATTTTTCA | ACCTTGCCAA | TCAAAGCGAT | GGTTGCTGCC | 650 |
| ATTCATCAGG | CTGGGCTTCC | TGCTTCTGTT | TCTAATACAG | CTGGTACCTT | 700 |
| TGTTTGCAAT | CATTTGATGT | ATCAAGCCCT | TTACTTAGTG | GATAAATATT | 750 |
| GTCCAAATGC | CAAAGCTGGG | TTTATGCATA | TTCCCTTTAT | GATGGAACAG | 800 |
| GTTGTTGATA | AACCTAATAC | AGCTGCCATG | AACCTCGATG | ATATTACAAG | 850 |
| AGGAATTGAG | GCTGCTATTT | TTGCCATTGT | CGATTTCAAA | GATCGTTCCG | 900 |
| ATTTAAAACG | TGTAGGGGGC | GCTACTCACT | GACTGTGACG | CTACTAAACC | 950 |
| TATTTTAAAA | AAACAGAGAT | ATGAACTAAC | TCTGTTTTTT | TTGTGCTAAA | 1000 |
| AATGAAAGAC | CTAGGGAAAC | TTTTCATCGG | TCTTTCTCAA | TTGTCATCTT | 1050 |
| AATCTAATAC | TACTTCTAAC | ATCAGCGGGT | ATAGTTTGCC | AGTAATTAAG | 1100 |
| AAACGTTGTT | GATCTAAATG | AGCAATCCCA | TTCAAAACAT | TAAGGTCAGG | 1150 |
| GTAATGGGAC | TTATCAAGAT | TTAAGGCTTT | TAACAAAGGA | CTAATATCAT | 1200 |
| AGGTGGCTAC | CACCTTTCCA | GAATCAGGTT | GGAGTTTGAC | AATAGTATTG | 1250 |
| GTTTGCCAAA | TATTGGCATA | GAGATAACCA | TCTACATACT | CTAATTCGTT | 1300 |
| AAGCATTGAG | ATAGGGACAC | TTTCTATAGC | AAC TAGT | | 1337 |

SIIRSTITUTE SHEET

92

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1837 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

| | | | | | |
|------------|------------|------------|-------------|-------------|------|
| TCATGTTTGA | CAGCTTATCA | TCGATAAGCT | TACTTTTTCGA | ATCAGGTCTA | 50 |
| TCCTTGAAAC | AGGTGCAACA | TAGATTAGGG | CATGGAGATT | TACCAGACAA | 100 |
| CTATGAACGT | ATATACTCAC | ATCACGCAAT | CGGCAATTGA | TGACATTGGA | 150 |
| ACTAAATTCA | ATCAATTTGT | TACTAACAAG | CAACTAGATT | GACAACTAAT | 200 |
| TCTCAACAAA | CGTTAATTTA | ACAACATTCA | AGTAACTCCC | ACCAGCTCCA | 250 |
| TCAATGCTTA | CCGTAAGTAA | TCATAACTTA | CTAAAACCTT | GTTACATCAA | 300 |
| GGTTTTTTCT | TTTGTCTTG | TTCATGAGTT | ACCATAACTT | TCTATATTAT | 350 |
| TGACAACTAA | ATTGACAAC | CTTCAATTAT | TTTTCTGTCT | ACTCAAAGTT | 400 |
| TTCTTCATTT | GATATAGTCT | AATTCCACCA | TCACTTCTTC | CACTCTCTCT | 450 |
| ACCGTCACAA | CTTCATCATC | TCTCACTTTT | TCGTGTGGTA | ACACATAATC | 500 |
| AAATATCTTT | CCGTTTTTAC | GCACTATCGC | TACTGTGTCA | CCTAAAATAT | 550 |
| ACCCCTTATC | AATCGCTTCT | TTAAACTCAT | CTATATATAA | CATATTTTCAT | 600 |
| CCTCCTACCT | ATCTATTTCG | AAAAAGATAA | AAATAACTAT | TGTTTTTTTT | 650 |
| GTTATTTTAT | AATAAAATTA | TTAATATAAG | TTAATGTTTT | TTAAAAATAT | 700 |
| ACAATTTTAT | TCTATTTATA | GTTAGCTATT | TTTTCATTGT | TAGTAATATT | 750 |
| GGTGAATTGT | AATAACCTTT | TTAAATCTAG | AGGAGAACCC | AGATATAAAA | 800 |
| TGGAGGAATA | TTAATGGAAA | ACAATAAAAA | AGTATTGAAG | AAAATGGTAT | 850 |
| TTTTTGTTTT | AGTGACATTT | CTTGGAATAA | CAATCTCGCA | AGAGGTATTT | 900 |
| GCTCAACAAG | ACCCCGATCC | AAGCCAACCT | CACAGATCTA | GTTTAGTTAA | 950 |
| AAACCTTCAA | AATATATATT | TTCTTTATGA | GGGTGACCCT | GTTACTCACG | 1000 |
| AGAATGTGAA | ATCTGTTGAT | CAACTTTTAT | CTCACGATTT | AATATATAAT | 1050 |
| GTTTCAGGGC | CAAATTATGA | TAAATTAAAA | ACTGAACTTA | AGAACCAAGA | 1100 |
| GATGGCAACT | TTATTTAAGG | ATAAAAACGT | TGATATTTAT | GGTGTAGAAT | 1150 |
| ATTACCATCT | CTGTTATTTA | TGTGAAAATG | CAGAAAGGAG | TGCATGTATC | 1200 |
| TACGGAGGGG | TAACAAATCA | TGAAGGGAAT | CATTTAGAAA | TTCTTAAAAA | 1250 |
| GATAGTCGTT | AAAGTATCAA | TCGATGGTAT | CCAAAGCCTA | TCATTTGATA | 1300 |

SUBSTITUTE SHEET

93

| | | | | | |
|------------|------------|------------|------------|------------|------|
| TTGAAACAAA | TAAAAAATG | GTAAGTCTC | AAGAATTAGA | CTATAAAGTT | 1350 |
| AGAAAATATC | TTACAGATAA | TAAGCAACTA | TATACTAATG | GACCTTCTAA | 1400 |
| ATATGAAACT | GGATATATAA | AGTTCATACC | TAAGAATAAA | GAAAGTTTTT | 1450 |
| GGTTTGATTT | TTTCCCTGAA | CCAGAATTTA | CTCAATCTAA | ATATCTTATG | 1500 |
| ATATATAAAG | ATAATGAAAC | GCTTGACTCA | AACACAAGCC | AAATTGAAGT | 1550 |
| CTACCTAACA | ACCAAGTAAC | TTTTTGCTTT | TGGCAACCTT | ACCTACTGCT | 1600 |
| GGATTTAGAA | ATTTTATTGC | AATTCTTTTA | TTAATGTAAA | AACCGCTCAT | 1650 |
| TTGATGAGCG | GTTTTGTCTT | ATCTAAAGGA | GCTTTACCTC | CTAATGCTGC | 1700 |
| AAAATTTTAA | ATGTTGGATT | TTTGTATTTG | TCTATTGTAT | TTGATGGGTA | 1750 |
| ATCCCATTTT | TCGACAGACA | TCGTCGTGCC | ACCTCTAACA | CCAAAATCAT | 1800 |
| AGACAGGAGC | TTGTAGCTTA | GCAACTATTT | TATCGTC | | 1837 |

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

| | | | | | |
|------------|------------|------------|-------------|------------|-----|
| GATCAATATG | TCCAAGAAAC | CACATGTTCC | TAAGACAAGA | GCTAACAGAC | 50 |
| TGGCCGTCOA | TAATAGTATT | GTTCTTTTTT | TCATCATTAC | TCCTTAACTA | 100 |
| GTGTTTAACT | GATTAATTAG | CCAGTAAATA | GTTTATCTTT | ATTTACACTA | 150 |
| TCTGTTAAGA | TATAGTAAAA | TGAAATAAGA | ACAGGACAGT | CAAATCGATT | 200 |
| TCTAACAATG | TTTTAGAAGT | AGAGGTATAC | TATTCTAATT | TCAATCTACT | 250 |
| ATATTTTGCA | CATTTTCATA | AAAAAATGA | GAAC TAGAAC | TCACATTCTG | 300 |
| CTCTCATTTT | TCGTTTTCCC | GTTCTCCTAT | CCTGTTTTTA | GGAGTTAGAA | 350 |
| AATGCTGCTA | CCTTTACTTA | CTCTCCTTTA | ATAAAGCCAA | TAGTTTTTCA | 400 |
| GCTTCTGCCA | TAATAGTATT | GTTGTCCTGG | GTGCCAAATA | GTAAATTATT | 450 |
| TTTTAATCCT | GTGAGAGTCT | CTTTGGCATT | GGACTTGATA | ATTGGATTCT | 500 |
| GGATTTTTCC | AAGTAAATCT | TCAGCCTCTC | TCAGTTTTCT | TAACCTTTCA | 550 |
| GTCTCGACCT | GAGGTTCTTC | TGATTCCTCT | GGTGATTCTT | CTGGTGATTC | 600 |
| TTCTTCTGGT | TCCTCTGTTG | GTTTTGGAGA | CTCTGGTTTC | TCGCTTTGCG | 650 |
| GTTTCTCTTC | TCGAGGGGTT | TCTTCCTCAG | GTTTTTCTGT | CTGAGGTTTC | 700 |
| TCCTCGTTTG | GTTTTCCCGT | TTGATTGGTA | TCAGCTTGAC | CATTTTTGTT | 750 |
| TCTTTGAACA | TGGTCGCTAG | CGTTACCAAA | ACCATTATCT | GAATGCGACG | 800 |

SUBSTITUTE SHEET

94

TTCGTTTGA TGTTCGACAT AGTACTTGAC AGTCGCCAAA A

841

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4500 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

| | | | | | |
|------------|------------|------------|------------|-------------|------|
| GATCAGGACA | GTCAAATCGA | TTTCTAACAA | TGTTTTAGAA | GATAGATGTGT | 50 |
| ACTATTCTAG | TTTCAATCTA | TTATATTTAT | AGAATTTTTT | GTTGCTAGAT | 100 |
| TTGTCAAATT | GCTTAAAATA | ATTTTTTTCA | GAAAGCAAAA | GCCGATACCT | 150 |
| ATCGAGTAGG | GTAGTTCCTG | CTATCGTCAG | GCTTGTCTGT | AGGTGTTAAC | 200 |
| ACTTTTCAAA | AATCTCTTCA | AACAACGTCA | GCTTTGCCCT | GCCGTATATA | 250 |
| TGTTACTGAC | TCGTCAGTT | CTATCTGCCA | CCTCAAAACG | GTGTTTTGAG | 300 |
| CTGACTTCGT | CAGTTCATC | CACAACCTCA | AAACAGTGTT | TTGAGCTGAC | 350 |
| TTCGTCAGTT | CTATCCACAA | CCTCAAAACA | GTGTTTTGAG | CTGACTTTGT | 400 |
| CAGTCTTATC | TACAACCTCA | AAACAGTGTT | TTGAGCATCA | TGCGGCTAGC | 450 |
| TTCTTAGTTT | GCTCTTTGAT | TTTCATTGAG | TATAAAAACA | GATGAGTTTC | 500 |
| TGTTTTCTTT | TTATGGACTA | TAAATGTTCA | GCTGAAACTA | CTTTCAAGGA | 550 |
| CATTATTATA | TAAAAGAATT | TTTTGAACT | AAAATCTACT | ATATTACACT | 600 |
| ATATTGAAAG | CGTTTTAAAA | ATGAGGTATA | ATAAATTTAC | TAACACTTAT | 650 |
| AAAAAGTGAT | AGAATCTATC | TTTATGTATA | TTTAAAGATA | GATTGCTGTA | 700 |
| AAAATAGTAG | TAGCTATGCG | AAATAACAGA | TAGAGAGAAG | GGATTGAAGC | 750 |
| TTAGAAAAGG | GGAATAATAT | GATATTTAAG | GCATTCAAGA | CAAAAAAGCA | 800 |
| GAGAAAAAGA | CAAGTTGAAC | TACTTTTGAC | AGTTTTTTTC | GACAGTTTTTC | 850 |
| TGATTGATTT | ATTTCTTCAC | TTATTTGGGA | TTGTCCCCCT | TAAGCTGGAT | 900 |
| AAGATTCTGA | TTGTGAGCTT | GATTATATTT | CCCATTATTT | CTACAAGTAT | 950 |
| TTATGCTTAT | GAAAAGCTAT | TTGAAAAAGT | GTTGATAAAG | GATTGAGCAG | 1000 |
| GAAGTATGGT | GTAAATAGCA | TAAGCTGATG | TCCATCATTT | GCTTATAAAG | 1050 |
| AGATATTTTA | GTTTAATTGC | AGCGGTGTCC | TGGTAGATAA | ACTAGATTGG | 1100 |
| CAGGAGTCTG | ATTGGAGAAA | GGAGAGGGGA | AATTTGGCAC | CAATTTGAGA | 1150 |
| TAGTTTGTTT | AGTTCATTTT | TGTCATTTAA | ATGAACTGTA | GTAAAAGAAA | 1200 |
| GTTAATAAAA | GACAAACTAA | GTGCATTTTC | TGGAATAAAT | GTCTTATTTT | 1250 |
| AGAAATCGGG | ATATAGATAT | AGAGAGGAAC | AGTATGAATC | GGAGTGTTCA | 1300 |

SUBSTITUTE SHEET

95

| | | | | | |
|-------------|------------|-------------|------------|-------------|------|
| AGAACGTAAG | TGTCGTTATA | GCATTAGGAA | ACTATCGGTA | GGAGCGGTTT | 1350 |
| CTATGATTGT | AGGAGCAGTG | GTATTTGGAA | CGTCTCCTGT | TTTAGCTCAA | 1400 |
| GAAGGGGCAA | GTGAGCAACC | TCTGGCAAAT | GAAACTCAAC | TTTCGGGGGA | 1450 |
| GAGCTCAACC | CTAACTGATA | CAGAAAAGAG | CCAGCCTTCT | TCAGAGACTG | 1500 |
| AACTTTCCTGG | CAATAAGCAA | GAACAAGAAA | GGAAAGATAA | GCAAGAAGAA | 1550 |
| AAAATTCCAA | GAGATTACTA | TGCACGAGAT | TTGGAAAATG | TCGAAACAGT | 1600 |
| GATAGAAAAA | GAAGATGTTG | AAACCAATGC | TTCAAATGGT | CAGAGAGTTG | 1650 |
| ATTTATCAAG | TGAACTAGAT | AAACTAAAGA | AACTTGAAAA | CGCAACAGTT | 1700 |
| CACATGGAGT | TTAAGCCAGA | TGCCAAGGCC | CCAGCATTCT | ATAATCTCTT | 1750 |
| TTCTGTGTCA | AGTGCTACTA | AAAAAGATGA | GTACTTCACT | ATGGCAGTTT | 1800 |
| ACAATAATAC | TGCTACTCTA | GAGGGGCGTG | GTTCGGATGG | GAAACAGTTT | 1850 |
| TACAATAATT | ACAACGATGC | ACCCTTAAAA | GTAAACCAG | GTCAGTGGAA | 1900 |
| TTCTGTGACT | TTCACAGTTG | AAAAACCGAC | AGCAGAACTA | CCTAAAGGCC | 1950 |
| GAGTGCGCCT | CTACGTAAAC | GGGGTATTAT | CTCGAACAAG | TCTGAGATCT | 2000 |
| GGCAATTTCA | TTAAAGATAT | GCCAGATGTA | ACGCATGTGC | AAATCGGAGC | 2050 |
| AACCAAGCGT | GCCAACAATA | CGGTTTGGGG | GTCAAATCTA | CAGATTCGGA | 2100 |
| ATCTCACTGT | GTATAATCGT | GCTTTAACAC | CAGAAGAGGT | ACAAAAACGT | 2150 |
| AGTCAACTTT | TTAAACGCTC | AGATTTAGAA | AAAAAACTAC | CTGAAGGAGC | 2200 |
| GGCTTTAACA | GAGAAAACGG | ACATATTCTGA | AAGCGGGCGT | AACGGTAAAC | 2250 |
| CAAATAAAGA | TGGAATCAAG | AGTTATCGTA | TTCCAGCACT | TCTCAAGACA | 2300 |
| GATAAAGGAA | CTTTGATCGC | AGGTGCAGAT | GAACGCCGTC | TCCATTTCGAG | 2350 |
| TGACTGGGGT | GATATCGGTA | TGGTCATCAG | ACGTAGTGAA | GATAATGGTA | 2400 |
| AACTTGGGG | TGACCGAGTA | ACCATTACCA | ACTTACGTGA | CAATCCAAAA | 2450 |
| GCTTCTGACC | CATCGATCGG | TTCACCAAGT | AATATCGATA | TGGTGTGGT | 2500 |
| TCAAGATCCT | GAAACCAAAC | GAATCTTTTC | TATCTATGAC | ATGTTCCCAG | 2550 |
| AAGGGAAGGG | AATCTTTGGA | ATGTCTTCAC | AAAAAGAAGA | AGCCTACAAA | 2600 |
| AAAATCGATG | GAAAAACCTA | TCAAATCCTC | TATCGTGAAG | GAGAAAAGGG | 2650 |
| AGCTTATACC | ATTCGAGAAA | ATGGTACTGT | CTATACACCA | GATGGTAAGG | 2700 |
| CGACAGACTA | TCGCGTTGTT | GTAGATCCTG | TTAAACCAGC | CTATAGCGAC | 2750 |
| AAGGGGGATC | TATACAAGGG | TAACCAATTA | CTAGGCAATA | TCTACTTCAC | 2800 |
| AACAAACAAA | ACTTCTCCAT | TTAGAATTGC | CAAGGATAGC | TATCTATGGA | 2850 |
| TGTCCTACAG | TGATGACGAC | GGGAAGACAT | GGTCAGCGCC | TCAAGATATT | 2900 |
| ACTCCGATGG | TCAAAGCCGA | TTGGATGAAA | TTCTTGGGTG | TAGGTCCTGG | 2950 |
| AACAGGAATT | GTAATTCCGA | ATGGGCCTCA | CAAGGGACGG | ATTTTGATAC | 3000 |
| CGGTTTATAC | GACTAATAAT | GTATCTCACT | TAAATGGCTC | GCAATCTTCT | 3050 |
| CGTATCATCT | ATTCAGATGA | TCATGGAAAA | ACTTGGCATG | CTGGAGAAGC | 3100 |
| GGTCAACGAT | AACCGTCAGG | TAGACGGTCA | AAAGATCCAC | TCTTCTACGA | 3150 |

SUBSTITUTE SHEET

96

| | | | | | |
|-------------|------------|------------|-------------|-------------|------|
| TGAACAATAG | ACGTGCGCAA | AATACAGAAT | CAACGGTGGT | ACAACTAAAC | 3200 |
| AATGGAGATG | TTAAACTCTT | TATGCGTGGT | TTGACTGGAG | ATCTTCAGGT | 3250 |
| TGCTACAAGT | AAAGACGGAG | GAGTGACTTG | GGAGAAGGAT | ATCAAACGTT | 3300 |
| ATCCACAGGT | TAAAGATGTC | TATGTTCAAA | TGTCTGCTAT | CCATACGATG | 3350 |
| CACGAAGGAA | AAGAATACAT | CATCCTCAGT | AATGCAGGTG | GACCGAAACG | 3400 |
| TGAAAATGGG | ATGGTCCACT | TGGCACGTGT | CGAAGAAAAT | GGTGAGTTGA | 3450 |
| CTTGCGCTCAA | ACACAATCCA | ATTCAAAAAG | GAGAGTTTGC | CTATAATTCTG | 3500 |
| CTCCAAGAAT | TAGGAAATGG | GGAGTATGGC | ATCTTGATATG | AACATACTGA | 3550 |
| AAAAGGACAA | AATGCCTATA | CCCTATCATT | TAGAAAATTT | AATTGGGACT | 3600 |
| TTTTTGAGCAA | AGATCTGATT | TCTCTACCG | AAGCGAAAGT | GAAGCGAACT | 3650 |
| AGAGAGATGG | GCAAAGGAGT | TATTGGCTTG | GAGTTCGACT | CAGAAGTATT | 3700 |
| GGTCAACAAG | GCTCCAACCC | TTCAATTGGC | AAATGGTAAA | ACAGCACGCT | 3750 |
| TCATGACCCA | GTATGATACA | AAAACCCTCC | TATTTACAGT | GGATTCAGAG | 3800 |
| GATATGGGTC | AAAAAGTTAC | AGGTTTGGCA | GAAGGTGCAA | TTGAAAGTAT | 3850 |
| GCATAATTTA | CCAGTCTCTG | TGGCGGGCAC | TAAGCTTTTCG | AATGGAATGA | 3900 |
| ACGGAAGTGA | AGCTGCTGTT | CATGAAGTGC | CAGAATACAC | AGGCCCATTA | 3950 |
| GGGACATCCG | GCGAAGAGCC | AGCTCCAACA | GTCGAGAAGC | CAGAATACAC | 4000 |
| AGGCCCACTA | GGGACATCCG | GCGAAGAGCC | AGCCCCGACA | GTCGAGAAGC | 4050 |
| CAGAATACAC | AGGCCCACTA | GGGACAGCTG | GTGAAGAAGC | AGCTCCAACA | 4100 |
| GTCGAGAAGC | CAGAATTTAC | AGGGGGAGTT | AATGGTACAG | AGCCAGCTGT | 4150 |
| TCATGAAATC | GCAGAGTATA | AGGGATCTGA | TTGCTTGTA | ACTCTTACTA | 4200 |
| CAAAGAAGA | TTATACTTAC | AAAGCTCCTC | TTGCTCAGCA | GGCACTTCCT | 4250 |
| GAAACAGGAA | ACAAGGAGAG | TGACCTCCTA | GCTTCACTAG | GACTAACAGC | 4300 |
| TTTCTTCCTT | GGTCTGTTTA | CGCTAGGGAA | AAAGAGAGAA | CAATAAGAGA | 4350 |
| AGAATTCTAA | ACATTTGATT | TTGTAAAAAT | AGAAGGAGAT | AGCAGGTTTT | 4400 |
| CAAGCCTGCT | ATCTTTTTTT | GATGACATTC | AGGCTGATAC | GAAATCATAA | 4450 |
| GAGGTCTGAA | ACTACTTTCA | GAGTAGTCTG | TTCTATAAAA | TATAGTAGAT | 4500 |

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

SUBSTITUTE SHEET

97

| | | | | | |
|------------|-------------|-------------|------------|-------------|-----|
| GATCCAAGCT | TATCGATATC | ATCAAAAAGT | TGGCGAACCT | TTTCAAATTT | 50 |
| TGGTTCAAAT | TCTTGAGATG | TATAGAATTC | AAAATATTTA | CCATTTGCAT | 100 |
| AGTCTGATTG | CTCAAAGTCT | TGATACTTTT | CTCCACGCTC | TTTTGCAATT | 150 |
| TCCATTGAAC | GTTTCGATGGA | ATAATAGTTC | ATAATCATAA | AGAATATATT | 200 |
| AGCAAAGTCT | TTTGCTTCTT | CAGATTCATA | GCCAATTTTA | TTTTTAGCTA | 250 |
| GATAACCATG | TAAGTTCATT | ACTCCTAGTC | CAACAGAATG | TAGTTCACTA | 300 |
| TTCGCTTTTT | TTACACCTGG | TGCATTTTGA | ATATTTGCTT | CATCACTTAC | 350 |
| AACTGTAAGA | GCATCCATAC | CTGTGAACAC | AGAATCTCTG | AATTTACCTG | 400 |
| ATTCCATAAC | ATTCACTATA | TTCAATGAGC | CTAAGTTACA | TGAAATATCT | 450 |
| CTTTTAATTT | CATCTTCAAT | TCCATAGTCG | TTAATTACTG | ATGTCTCTTG | 500 |
| TAATTGGAAA | ATTTTCAGTAC | ATAAATTACT | CATTTTAATT | TGCCCCAATAT | 550 |
| TTGAATTTCG | ATGTACTTTG | TTTGCAATTAT | CTTTAAACAT | AAGATATGGA | 600 |
| TAACCAGACT | GTAATTGTGT | TTGTGCAATC | ATATTTAACA | TTTCACGTGC | 650 |
| GTCTTTTTTC | TTTTTATCGA | TTTCGAACCC | GGGGTACCGA | ATTCCTCGAG | 700 |
| TCTAG | | | | | 705 |

SUBSTITUTE SHEET

98

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| GATCAATCTT | TGTCGGTACA | CGATATTCTT | CACGACTAAA | TAAACGCTCA | 50 |
| TTCGCGATTT | TATAAATGAA | TGTTGATAAC | AATGTTGTAT | TATCTACTGA | 100 |
| AATCTCATT | CGTTGCATCG | GAAACATTGT | GTTCTGTATG | TAAAAGCCGT | 150 |
| CTTGATAATC | TTAGTAGTA | CCGAAGCTGG | TCATACGAGA | GTTATATTTT | 200 |
| CCAGCCAAAA | CGATATTTTT | ATAATCATT | CGTGAAAAAG | GTTTCCCTTC | 250 |
| ATTATCACAC | AAATATTTTA | GCTTTTCAGT | TTCTATATCA | ACTGTAGCTT | 300 |
| CTTTATCCAT | ACGTTGAATA | ATTGTACGAT | TCTGACGCAC | CATCTTTTGC | 350 |
| ACACCTTTAA | TGTTATTTGT | TTTAAAAGCA | TGAATAAGTT | TTTCAACACA | 400 |
| ACGATGTGAA | TCTTCTAAGA | AGTCACCGTA | AAATGAAGGA | TC | 442 |

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GCAATACAGG GAAAAATGTC

99

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTTCATCAAA CAATTAACTC

20

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GAACAGAAGA AGCCAAAAAA

20

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GCAATCCCAA ATAATACGGT

20

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET

100

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GCTTTCCAGC GTCATATTG

19

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GATCTCGACA AAATGGTGA

19

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CACCCGCTTG CGTGGCAAGC TGCCC

25

SUBSTITUTE SHEET

101

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CGTTTGTGGA TTCCAGTTCC ATCCG

25

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TCACCCGCTT GCGTGGC

17

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGAAGTGGAA TCCACAAAC

19

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases

SUBSTITUTE SHEET

102

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TGAAGCACTG GCCGAAATGC TCGGT

25

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GATGTACAGG ATTCGTTGAA GGCTT

25

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TAGCGAAGGC GTAGCAGAAA CTAAC

25

SUBSTITUTE SHEET

103

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GCAACCCGAA CTCAACGCCG GATTT

25

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

ATACACAAGG GTCGCATCTG CGGCC

25

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TGCGTATGCA TTGCAGACCT TGTGGC

26

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases

SUBSTITUTE SHEET

104

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GCTTTCACCTG GATATCGCGC TTGGG

25

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GCAACCCGAA CTCAACGCC

19

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GCAGATGCGA CCCTTGTGT

19

SUBSTITUTE SHEET

105

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GTGGTGTCGT TCAGCGCTTT CAC

23

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GCGATATTCA CACCCTACGC AGCCA

25

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GTCGAAAATG CCGGAAGAGG TATACG

26

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

106

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACTGAGCTGC AGACCGGTAA AACTCA

26

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAGTCAGT TCGTCAGCC

19

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CGTAGGGTGT GAATATCGC

19

SUBSTITUTE SHEET

107

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CGTGATGGAT ATTCTTAACG AAGGGC

26

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

ACCAAACGTG TGAGCCGCCT GGA

23

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GTGATCGCCC CTCATCTGCT ACT

23

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 bases

SUBSTITUTE SHEET

108

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CGCCCTTCGT TAAGAATATC CATCAC

26

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TCGCCCCTCA TCTGCTACT

19

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GATCGTGATG GATATTCTT

19

SUBSTITUTE SHEET

109

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CAGGAAGATG CTGCACCGGT TGTTG

25

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TGGTTCAGTG ACTTTGCGAT GTTTC

25

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TCGAGGATGG CATGCACTAG AAAAT

25

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

110

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CGCTGATTAG GTTTCGCTAA AATCTTATTA

30

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TTGATCCTCA TTTTATTAAT CACATGACCA

30

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GAAACATCGC AAAGTCAGT

19

SUBSTITUTE SHEET

111

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

ATAAAATGAG GATCAAGTTC

20

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CCGCCTTTAG CATTAATTGG TGTTTATAGT

30

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CCTATTGCAG ATACCTTAAA TGTCTTGGGC

30

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

112

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

AGTAAAATGA AATAAGAACA GGACAG

26

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AAAACAGGAT AGGAGAACGG GAAAA

25

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TTGAGTGATG ATTTACTGA CTCCC

25

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET

113

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GTCAGACAGT GATGCTGACG ACACA

25

- (2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

TGTTTGTTCAT GCTGTTTGTG TGAAAAT

27

- (2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGAGCGGGTG GTGTTCATC

19

SUBSTITUTE SHEET

M4

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CAAGTCGTCG TCGGAGGGA

19

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TCGCTGTTCA TCAAGACCC

19

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CCGAGAACCA GACTTCATC

19

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bas s
- (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

115

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AATGCGGCTG TACCTCGGCG CTGGT

25

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GGCGGAGGGC CAGTGCACC TGCCA

25

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

AGCCCTGCTC CTCGGCAGCC TCTGC

25

SUBSTITUTE SHEET

116

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas aeruginosa*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

TGGCTTTTGC AACCGCGTTC AGGT

25

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas aeruginosa*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

GCGCCCGCGA GGGCATGCTT CGATG

25

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas aeruginosa*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

ACCTGGGCGC CAACTACAAG TTCTA

25

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

117

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GGCTACGCTG CCGGGCTGCA GGCCG

25

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

CCGATCTACA CCATCGAGAT GGGCG

25

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

GAGCGCGGCT ATGTGTTTCGT CGGCT

25

118

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CGTTTTTACC CTTACCTTTT CGTACTACC

29

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TCAGGCAGAG GTAGTACGAA AAGGTAAGGG

30

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTTTTTACC CTTACCTTTT CGTACT

26

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

119

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATCGATCATC ACATTCCATT TGTTTTTA

28

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CACCAAGTTT GACACGTGAA GATTCAT

27

(2) INFORMATION FOR SEQ ID NO: 101

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

ATGAGTGAAG CGGAGTCAGA TTATGTGCAG

30

SUBSTITUTE SHEET

110

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGCTCATTAC GTACAGTGAC AATCG

25

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CTGGTTAGCT TGACTCTTAA CAATCTTGTC

30

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GACGCGATTG TCACTGTACG TAATGAGCGA

30

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

121

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GCGTCAGAAA AAGTAGGCGA AATGAAAG

28

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AGCGGCTCTA TCTTGTAATG ACACA

25

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GAAACGTGAA CTCCCCTCTA TATAA

25

SUBSTITUTE SHEET

122

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GCCCCAAAAC AATGAAACAT ATGGT

25

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CTGCAGATTT TGAATCATA TCGCC

25

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TG GTTTGACC AGTATTTAAC GCCAT

25

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

123

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CAACGGCACC TGATGTACCT TGTAC

25

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GGCACCTGAT GTACCTTG

18

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AACAGCTCAC ACGCATT

17

SUBSTITUTE SHEET

124

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

TTACAACCTG CACCACAAGT CATCA

25

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GTACAAACAA GCCGTCAGCG ACTTA

25

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CAATCTGCGT GTGTGCGTTC ACT

23

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

125

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GCTACTTTGT CAGCTTTAGC CATTCA

26

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

TGTTTTGAGC TTTTATTTT TTGA

24

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CGCTGACGGC TTGTTGTAC CA

22

SUBSTITUTE SHEET

126

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

TCTGTGCTAG AGACTGCCCC ATTTC

25

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

CGATGTCTTG ATTGAGCAGG GTTAT

25

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ATCCCACCTT AGGCGGCTGG CTCCA

25

127

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ACGTCAAGTC ATCATGGCCC TTACGAGTAG G

31

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GTGTGACGGG CGGTGTGTAC AAGGC

25

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GAGTTGCAGA CTCCAATCCG GACTACGA

28

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GGAGGAAGGT GGGGATGACG

20

SUBSTITUTE SHEET

128

(2) INFORMATION FOR SEQ ID NO: 127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

ATGGTGTGAC GGGCGGTGTG

20

(2) INFORMATION FOR SEQ ID NO: 128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CCCTATACAT CACCTTGCGG TTTAGCAGAG AG

32

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GGGGGGACCA TCCTCCAAGG CTAAATAC

28

SUBSTITUTE SHEET

129

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CGTCCACTTT CGTGTTTGCA GAGTGCTGTG TT

32

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

CAGGAGTACG GTGATTTTTA

20

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

ATTTCTGGTT TGGTCATACA

20

SUBSTITUTE SHEET

130

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CGGGAGTCAG TGAAATCATC

20

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CTAAAATCGC CACACCTCTT

20

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

GCAGCGTGGT GTCGTTCA

18

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

131

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGCTGGCAAC GGCTGGTC

18

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

ATTCACACCC TACGCAGCCA

20

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

ATCCGGCAGC ATCTCTTTGT

20

SUBSTITUTE SHEET

132

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CTGGTTAGCT TGACTCTTAA CAATC

25

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TCTTAACGAT AGAATGGAGC AACTG

25

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGAAAATTCT TGTAACAGGC

20

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid

SEQUENCE SHEET

133

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

GGCCACCAGC TTGCCCAATA

20

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATATTTTCTT TATGAGGGTG

20

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

ATCCTTAAAT AAAGTTGCCA

20

SUBSTITUTE SHEET

134

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

ATCAAAAAGT TGGCGAACCT TTTCA

25

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

CAAAAGAGCG TGGAGAAAAG TATCA

25

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

TCTCTTTTAA TTTCATCTTC AATTCATAG

30

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

135

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

AAACACAATT ACAGTCTGGT TATCCATATC

30

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

CTTCATTTTA CGGTGACTTC TTAGAAGATT

30

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TCAACTGTAG CTTCTTTATC CATACGTTGA

30

SUBSTITUTE SHEET

136

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATATTTTAGC TTTTCAGTTT CTATATCAAC

30

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

AATCTTTGTC GGTACACGAT ATTCTTCACG

30

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

CGTAATGAGA TTTCAGTAGA TAATACAACA

30

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

SUBSTITUTE SHEET

137

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

TTTAACGATC CTTTACTCC TTTTG

25

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ACTGCTGTTG TAAAGAGGTT AAAAT

25

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

ATTTGGTGAC GGGTGACTTT

20

SUBSTITUTE SHEET

138

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GCTGAGGATT TGTTCTTCTT

20

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GAGCGGTTTC TATGATTGTA

20

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

ATCTTTCCTT TCTTGTTCTT

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid

SUBSTITUTE SHEET

139

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

GCTCAAATCA GGGTCAGC

18

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

| | | | | | |
|-------------|------------|------------|------------|------------|-----|
| ATGAGTATTC | AACATTTCCG | TGTCGCCCTT | ATTCCCTTTT | TTGCGGCATT | 50 |
| TTGCCCTTCCT | GTTTTTGCTC | ACCCAGAAAC | GCTGGTGAAA | GTAAAAGATG | 100 |
| CTGAAGATCA | GTTGGGTGCA | CGAGTGGGTT | ACATCGAACT | GGATCTCAAC | 150 |
| AGCGGTAAGA | TCCTTGAGAG | TTTTCGCCCC | GAAGAACGTT | TTCCAATGAT | 200 |
| GAGCACTTTT | AAAGTTCTGC | TATGTGGCGC | GGTATTATCC | CGTGTTGACG | 250 |
| CCGGGCAAGA | GCAACTCGGT | CGCCGCATAC | ACTATTCTCA | GAATGACTTG | 300 |
| GTTGAGTACT | CACCAGTCAC | AGAAAAGCAT | CTTACGGATG | GCATGACAGT | 350 |
| AAGAGAATTA | TGCAGTGCTG | CCATAACCAT | GAGTGATAAC | ACTGCGGCCA | 400 |
| ACTTACTTCT | GACAACGATC | GGAGGACCGA | AGGAGCTAAC | CGCTTTTTTG | 450 |
| CACAACATGG | GGGATCATGT | AACTCGCCTT | GATCGTTGGG | AACCGGAGCT | 500 |
| GAATGAAGCC | ATACCAAACG | ACGAGCGTGA | CACCACGATG | CCTGCAGCAA | 550 |
| TGGCAACAAC | GTTGCGCAAA | CTATTAACTG | GCGAACTACT | TACTCTAGCT | 600 |
| TCCCGGCAAC | AATTAATAGA | CTGGATGGAG | GCGGATAAAG | TTGCAGGACC | 650 |
| ACTTCTGCGC | TCGGCCCTTC | CGGCTGGCTG | GTTTATTGCT | GATAAATCTG | 700 |
| GAGCCGGTGA | GCGTGGGTCT | CGCGGTATCA | TTGCAGCACT | GGGGCCAGAT | 750 |
| GGTAAGCCCT | CCCGTATCGT | AGTTATCTAC | ACGACGGGGA | GTCAGGCAAC | 800 |
| TATGGATGAA | CGAAATAGAC | AGATCGCTGA | GATAGGTGCC | TACTGATTA | 850 |
| AGCATTGGTA | A | | | | 861 |

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET

140

- (A) LENGTH: 918 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```

ATGTTAAATA AGTTAAAAAT CGGCACATTA TTATTGCTGA CATTAACGGC 50
TTGTTGCCCC AATTCTGTTC ATTCGGTAAC GTCTAATCCG CAGCCTGCTA 100
GTGCGCCTGT GCAACAATCA GCCACACAAG CCACCTTTCA ACAGACTTTG 150
GCGAATTTGG AACAGCAGTA TCAAGCCCGA ATTGGCGTTT ATGTATGGGA 200
TACAGAAACG GGACATTCTT TGTCTTATCG TGCAGATGAA CGCTTTGCTT 250
ATGCGTCCAC TTTCAAGGCG TTGTTGGCTG GGGCGGTGTT GCAATCGCTG 300
CCTGAAAAAG ATTTAAATCG TACCATTTCA TATAGCCAAA AAGATTTGGT 350
TAGTTATTCT CCCGAAACCC AAAAATACGT TGGCAAAGGC ATGACGATTG 400
CCCAATTATG TGAAGCAGCC GTGCGGTTTA GCGACAACAG CGCGACCAAT 450
TTGCTGCTCA AAGAATTGGG TGGCGTGGAA CAATATCAAC GTATTTTGCG 500
ACAATTAGGC GATAACGTAA CCCATACCAA TCGGCTAGAA CCCGATTTAA 550
ATCAAGCCAA ACCCAACGAT ATTCGTGATA CGAGTACACC CAAACAAATG 600
GCGATGAATT TAAATGCGTA TTTATTGGGC AACACATTAA CCGAATCGCA 650
AAAAACGATT TTGTGGAATT GGTGAGCAA TAACGCAACA GGCAATCCAT 700
TGATTCGCGC TGCTACGCCA ACATCGTGGA AAGTGACGA TAAAAGCGGG 750
GCGGGTAAAT ATGGTGTACG CAATGATATT GCGGTGGTTC GCATACCAA 800
TCGCAAACCG ATTGTGATGG CAATCATGAG TACGCAATTT ACCGAAGAAG 850
CCAAATTCAA CAATAAATTA GTAGAAGATG CAGCAAAGCA AGTATTTTCAT 900
ACTTTACAGC TCAACTAA                                     918

```

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```

ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT 50
GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA 100
GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC 150

```

SUBSTITUTE SHEET

141

| | | | | | |
|------------|------------|-------------|------------|-------------|-----|
| CGCACGCTGA | CCGCCTGGCG | CGCCGATGAA | CGCTTTCCCA | TGATGAGCAC | 200 |
| CTTTAAAGTA | GTGCTCTGCG | GCGCAGTGCT | GGCGCGGGTG | GATGCCGGTG | 250 |
| ACGAACAGCT | GGAGCGAAAG | ATCCACTATC | GCCAGCAGGA | TCTGGTGGAC | 300 |
| TACTCGCCGG | TCAGCGAAAA | ACACCTTGCC | GACGCAATGA | CGGTCGGCGA | 350 |
| ACTCTGCGCC | GCCGCCATTA | CCATGAGCGA | TAACAGCGCC | GCCAATCTGC | 400 |
| TACTGGCCAC | CGTCGGCGGC | CCCGCAGGAT | TGACTGCCTT | TTTGCGCCAG | 450 |
| ATCGGCGACA | ACGTCAACCG | CCTTGACCGC | TGGGAAACGG | AACTGAATGA | 500 |
| GGCGCTTCCC | GGCGACGCCC | GCGACACCAC | TACCCCGGCC | AGCATGGCCG | 550 |
| CGACCCTGCG | CAACGTTGGC | CTGACCAGCC | AGCGTCTGAG | CGCCCGTTTCG | 600 |
| CAACGGCAGC | TGCTGCAGTG | GATGGTGGAC | GATCGGGTCG | CCGGACCGTT | 650 |
| GATCCGCTCC | GTGCTGCCGG | CGGGCTGGTT | TATCGCCGAT | AAGACCGGAG | 700 |
| CTGGCGAGCG | GGGTGCGCGC | GGGATTGTCTG | CCCTGCTTGG | CCCGAATAAC | 750 |
| AAAGCAGAGC | GCATTGTGGT | GATTTATCTG | CGGGATACCC | CGGCGAGCAT | 800 |
| GGCCGAGCGA | AATCAGCAAA | TCGCCGGGAT | CGGCAAGGCG | CTGTACGAGC | 850 |
| ACTGGCAACG | CTAA | | | | 864 |

(2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATGGACACAA | CGCAGGTCAC | ATTGATACAC | AAAATTCTAG | CTGCGGCAGA | 50 |
| TGAGCGAAAT | CTGCCGCTCT | GGATCGGTGG | GGGCTGGGCG | ATCGATGCAC | 100 |
| GGCTAGGGCG | TGTAACACGC | AAGCACGATG | ATATTGATCT | GACGTTTCCC | 150 |
| GGCGAGAGGC | GCGGCGAGCT | CGAGGCAATA | GTTGAAATGC | TCGGCGGGCG | 200 |
| CGTCATGGAG | GAGTTGGACT | ATGGATTCTT | AGCGGAGATC | GGGGATGAGT | 250 |
| TACTTGACTG | CGAACCTGCT | TGGTGGGCAG | ACGAAGCGTA | TGAAATCGCG | 300 |
| GAGGCTCCGC | AGGGCTCGTG | CCCAGAGGCG | GCTGAGGGCG | TCATCGCCCG | 350 |
| GCGGCCAGTC | CGTTGTAAAC | GCTGGGAGGC | GATCATCTGG | GATTACTTTT | 400 |
| ACTATGCCGA | TGAAGTACCA | CCAGTGGACT | GGCCTACAAA | GCACATAGAG | 450 |
| TCCTACAGGC | TCGCATGCAC | CTCACTCGGG | GCGGAAAAGG | TTGAGGTCTT | 500 |
| GCGTGCCGCT | TTCAGGTCGC | GATATGCGGC | CTAA | | 534 |

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET

142

- (A) LENGTH: 465 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```

ATGGGCATCA TTCGCACATG TAGGCTCGGC CCTGACCAAG TCAAATCCAT 50
GCGGGCTGCT CTTGATCTTT TCGGTCGTGA GTTCGGAGAC GTAGCCACCT 100
ACTCCCAACA TCAGCCGGAC TCCGATTACC TCGGGAACCT GCTCCGTAGT 150
AAGACATTCA TCGCGCTTGC TGCCTTCGAC CAAGAAGCGG TTGTTGGCGC 200
TCTCGCGGCT TACGTTCTGC CCAGGTTTGA GCAGCCGCGT AGTGAGATCT 250
ATATCTATGA TCTCGCAGTC TCCGGCGAGC ACCGGAGGCA GGGCATTGCC 300
ACCGCGCTCA TCAATCTCCT CAAGCATGAG GCCAACGCGC TTGGTGCTTA 350
TGTGATCTAC GTGCAAGCAG ATTACGGTGA CGATCCCGCA GTGGCTCTCT 400
ATACAAAGTT GGGCATACGG GAAGAAGTGA TGCACTTTGA TATCGACCCA 450
AGTACCGCCA CCTAA 465

```

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 861 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```

ATGCATACGC GGAAGGCAAT AACGGAGGCG CTTCAAAAAC TCGGAGTCCA 50
AACCGGTGAC CTATTGATGG TGCATGCCTC ACTTAAAGCG ATTGGTCCGG 100
TCGAAGGAGG AGCGGAGACG GTCGTTGCCG CGTTACGCTC CGCGGTTGGG 150
CCGACTGGCA CTGTGATGGG ATACGCATCG TGGGACCGAT CACCCTACGA 200
GGAGACTCGT AATGGCGCTC GGTGATGA CAAAACCCGC CGTACCTGGC 250
CGCCGTTCTGA TCCCGCAACG GCCGGGACTT ACCGTGGGTT CGGCCTGCTG 300
AATCAGTTTC TGGTTCAAGC CCCC GGCGCG CGGCGCAGCG CGCACCCCGA 350
TGCATCGATG GTCGCGGTTG GTCCACTGGC TGAAACGCTG ACGGAGCCTC 400
ACAAGCTCGG TCACGCCTTG GGGGAAGGGT CGCCCGTCGA GCGGTTCTGTT 450
CGCCTTGGCG GGAAGGCCCT GCTGTTGGGT GCGCCGCTAA ACTCCGTTAC 500
CGCATTGCAC TACGCCGAGG CGGTTGCCGA TATCCCCAAC AAACGGCGGG 550
TGACGTATGA GATGCCGATG CTTGGAAGCA ACGGCGAAGT CGCCTGGAAA 600

```

SUBSTITUTE SHEET

A43

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ACGGCATCGG | ATTACGATTC | AAACGGCATT | CTCGATTGCT | TTGCTATCGA | 650 |
| AGGAAAGCCG | GATGCGGTCG | AAACTATAGC | AAATGCTTAC | GTGAAGCTCG | 700 |
| GTCGCCATCG | AGAAGGTGTC | GTGGGCTTTG | CTCAGTGCTA | CCTGTTCGAC | 750 |
| GCGCAGGACA | TCGTGACGTT | CGGCGTCACC | TATCTTGAGA | AGCATTTCGG | 800 |
| AACCACTCCG | ATCGTGCCAG | CACACGAAGT | CGCCGAGTGC | TCTTGCGAGC | 850 |
| CTTCAGGTTA | G | | | | 861 |

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATGACCGATT | TGAATATCCC | GCATACACAC | GCGCACCTTG | TAGACGCATT | 50 |
| TCAGGCGCTC | GGCATCCGCG | CGGGGCAGGC | GCTCATGCTG | CACGCATCCG | 100 |
| TTAAAGCAGT | GGGCGCGGTG | ATGGGCGGCC | CCAATGTGAT | CTTGCAGGCG | 150 |
| CTCATGGATG | CGCTCACGCC | CGACGGCACG | CTGATGATGT | ATGCGGGATG | 200 |
| GCAAGACATC | CCCGACTTTA | TCGACTCGCT | GCCGGACGCG | CTCAAGGCCG | 250 |
| TGTATCTTGA | GCAGCACCCA | CCCTTTGACC | CCGCCACCGC | CCGCGCCGTG | 300 |
| CGCGAAAACA | GCGTGCTAGC | GGAATTTTGT | CGCACATGGC | CGTGCGTGCA | 350 |
| TCGCAGCGCA | AACCCCGAAG | CCTCTATGGT | GGCGGTAGGC | AGGCAGGCCG | 400 |
| CTTTGCTGAC | CGCTAATCAC | GCGCTGGATT | ATGGCTACGG | AGTCGAGTCG | 450 |
| CCGCTGGCTA | AACTGGTGCC | AATAGAAGGA | TACGTGCTGA | TGCTTGCGCG | 500 |
| GCCGCTGGAT | ACCATCACAC | TGCTGCACCA | CGCGGAATAT | CTGGCCAAGA | 550 |
| TGCGCCACAA | GAACGTGGTC | CGCTACCCGT | GCCCGATTCT | GCGGGACGGG | 600 |
| CGCAAAGTGT | GGGTGACCGT | TGAGGACTAT | GACACCGGTG | ATCCGCACGA | 650 |
| CGATTATAGT | TTTGAGCAAA | TCGCGCGCGA | TTATGTGGCG | CAGGGCGGCG | 700 |
| GCACACGCGG | CAAAGTCGGT | GATGCGGATG | CTTACCTGTT | CGCCGCGCAG | 750 |
| GACCTCACAC | GGTTTGCGGT | GCAGTGGCTT | GAATCACGGT | TCGGTGACTC | 800 |
| AGCGTCATAC | GGATAG | | | | 816 |

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

SUBSTITUTE SHEET

144

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

| | | | | | |
|------------|-------------|------------|------------|------------|-----|
| ATGCTCTATG | AGTGGCTAAA | TCGATCTCAT | ATCGTCGAGT | GGTGGGGCGG | 50 |
| AGAAGAAGCA | CGCCCGACAC | TTGCTGACGT | ACAGGAACAG | TACTTGCCAA | 100 |
| GCGTTTTAGC | GCAAGAGTCC | GTCACTCCAT | ACATTGCAAT | GCTGAATGGA | 150 |
| GAGCCGATTG | GGTATGCCCA | GTCGTACGTT | GCTCTTGGA | GCGGGGACGG | 200 |
| ATGGTGGGAA | GAAGAAACCG | ATCCAGGAGT | ACGCGGAATA | GACCAGTTAC | 250 |
| TGGCGAATGC | ATCACAACCTG | GGCAAAGGCT | TGGGAACCAA | GCTGGTTCGA | 300 |
| GCTCTGGTTG | AGTTGCTGTT | CAATGATCCC | GAGGTCACCA | AGATCCAAAC | 350 |
| GGACCCGTCG | CCGAGCAACT | TGCGAGCGAT | CCGATGCTAC | GAGAAAGCGG | 400 |
| GGTTTGAGAG | GCAAGGTACC | GTAACCACCC | CAGATGGTCC | AGCCGTGTAC | 450 |
| ATGGTTCAAA | CACGCCAGGC | ATTCGAGCGA | ACACGCAGTG | ATGCCTAA | 498 |

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATGAAAAAGA | TAAAAATTGT | TCCACTTATT | TTAATAGTTG | TAGTTGTCGG | 50 |
| GTTTGGTATA | TATTTTTATG | CTTCAAAGA | TAAAGAAATT | AATAATACTA | 100 |
| TTGATGCAAT | TGAAGATAAA | AATTTCAAAC | AAGTTTATAA | AGATAGCAGT | 150 |
| TATATTTCTA | AAAGCGATAA | TGGTGAAGTA | GAAATGACTG | AACGTCCGAT | 200 |
| AAAAATATAT | AATAGTTTAG | GCGTTAAAGA | TATAAACATT | CAGGATCGTA | 250 |
| AAATAAAAAA | AGTATCTAAA | AATAAAAAAC | GAGTAGATGC | TCAATATAAA | 300 |
| ATTAAAACAA | ACTACGGTAA | CATTGATCGC | AACGTTCAAT | TTAATTTTGT | 350 |
| TAAAGAAGAT | GGTATGTGGA | AGTTAGATTG | GGATCATAGC | GTCATTATTC | 400 |
| CAGGAATGCA | GAAAGACCAA | AGCATACATA | TTGAAAATTT | AAAATCAGAA | 450 |
| CGTGGTAAAA | TTTTAGACCG | AAACAATGTG | GAATTGGCCA | ATACAGGAAC | 500 |
| ACATATGAGA | TTAGGCATCG | TTCCAAAGAA | TGTATCTAAA | AAAGATTATA | 550 |
| AAGCAATCGC | TAAAGAACTA | AGTATTTCTG | AAGACTATAT | CAACAACAAA | 600 |
| TGGATCAAAA | TTGGGTACAA | GATGATACCT | TCGTTCCACT | TTAAAACCGT | 650 |
| TAAAAAAATG | GATGAATATT | TAAGTGATTT | CGCAAAAAAA | TTTCATCTTA | 700 |
| CAACTAATGA | AACAGAAAGT | CGTAACTATC | CTCTAGAAAA | AGCGACTTCA | 750 |
| CATCTATTAG | GTTATGTTGG | TCCCATTAAC | TCTGAAGAAT | TAAAACAAAA | 800 |

SUBSTITUTE SHEET

145

| | | | | | |
|------------|------------|------------|------------|------------|------|
| AGAATATAAA | GGCTATAAAG | ATGATGCAGT | TATTGGTAAA | AAGGGACTCG | 850 |
| AAAAACTTTA | CGATAAAAAG | CTCCAACATG | AAGATGGCTA | TCGTGTCACA | 900 |
| ATCGTTGACG | ATAATAGCAA | TACAATCGCA | CATACATTAA | TAGAGAAAAA | 950 |
| GAAAAAAGAT | GGCAAAGATA | TTCAACTAAC | TATTGATGCT | AAAGTTCAAA | 1000 |
| AGAGTATTTA | TAACAACATG | AAAAATGATT | ATGGCTCAGG | TACTGCTATC | 1050 |
| CACCCTCAAA | CAGGTGAATT | ATTAGCACTT | GTAAGCACAC | CTTCATATGA | 1100 |
| CGTCTATCCA | TTTATGTATG | GCATGAGTAA | CGAAGAATAT | AATAAATTAA | 1150 |
| CCGAAGATAA | AAAAGAACCT | CTGCTCAACA | AGTTCCAGAT | TACAACTTCA | 1200 |
| CCAGGTTCAA | CTCAAAAAAT | ATTAACAGCA | ATGATTGGGT | TAAATAACAA | 1250 |
| AACATTAGAC | GATAAAACAA | GTTATAAAAT | CGATGGTAAA | GGTTGGCAAA | 1300 |
| AAGATAAATC | TTGGGGTGGT | TACAACGTTA | CAAGATATGA | AGTGGTAAAT | 1350 |
| GGTAATATCG | ACTTAAAACA | AGCAATAGAA | TCATCAGATA | ACATTTTCTT | 1400 |
| TGCTAGAGTA | GCACTCGAAT | TAGGCAGTAA | GAAATTTGAA | AAAGGCATGA | 1450 |
| AAAAACTAGG | TGTTGGTGAA | GATATACCAA | GTGATTATCC | ATTTTATAAT | 1500 |
| GCTCAAATTT | CAAACAAAAA | TTTAGATAAT | GAAATATTAT | TAGCTGATTC | 1550 |
| AGGTTACGGA | CAAGGTGAAA | TACTGATTAA | CCCAGTACAG | ATCCTTTCAA | 1600 |
| TCTATAGCGC | ATTAGAAAAT | AATGGCAATA | TTAACGCACC | TCACTTATTA | 1650 |
| AAAGACACGA | AAAACAAAGT | TTGGAAGAAA | AATATTATTT | CCAAAGAAAA | 1700 |
| TATCAATCTA | TTAAATGATG | GTATGCAACA | AGTCGTAAAT | AAAACACATA | 1750 |
| AAGAAGATAT | TTATAGATCT | TATGCAAAC | TAATTGGCAA | ATCCGGTACT | 1800 |
| GCAGAACTCA | AAATGAAACA | AGGAGAAAGT | GGCAGACAAA | TTGGGTGGTT | 1850 |
| TATATCATAT | GATAAAGATA | ATCCAAACAT | GATGATGGCT | ATTAATGTTA | 1900 |
| AAGATGTACA | AGATAAAGGA | ATGGCTAGCT | ACAATGCCAA | AATCTCAGGT | 1950 |
| AAAGTGTATG | ATGAGCTATA | TGAGAACGGT | AATAAAAAAT | ACGATATAGA | 2000 |
| TGAATAA | | | | | 2007 |

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2607 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATGAATAACA | TCGGCATTAC | TGTTTATGGA | TGTGAGCAGG | ATGAGGCAGA | 50 |
| TGCATTCCAT | GCTCTTTCGC | CTCGCTTTGG | CGTTATGGCA | ACGATAATTA | 100 |
| ACGCCAACGT | GTCGGAATCC | AACGCCAAAT | CCGCGCCTTT | CAATCAATGT | 150 |
| ATCAGTGTGG | GACATAAATC | AGAGATTTC | GCCTCTATTG | TTCTTTCGCT | 200 |

SUBSTITUTE SHEET

A46

| | | | | | |
|------------|------------|------------|------------|------------|------|
| GAAGAGAGCC | GGTGTGAAAT | ATATTTCTAC | CCGAAGCATC | GGCTGCAATC | 250 |
| ATATAGATAC | AACTGCTGCT | AAGAGAATGG | GCATCACTGT | CGACAATGTG | 300 |
| GCGTACTCGC | CGGATAGCGT | TGCCGATTAT | ACTATGATGC | TAATTCTTAT | 350 |
| GGCAGTACGC | AACGTAAAAT | CGATTGTGCG | CTCTGTGGAA | AAACATGATT | 400 |
| TCAGGTTGGA | CAGCGACCGT | GGCAAGGTAC | TCAGCGACAT | GACAGTTGGT | 450 |
| GTGGTGGGAA | CGGGCCAGAT | AGGCAAAGCG | GTTATTGAGC | GGCTGCGAGG | 500 |
| ATTTGGATGT | AAAGTGTTGG | CTTATAGTCG | CAGCCGAAGT | ATAGAGGTAA | 550 |
| ACTATGTACC | GTTTGATGAG | TTGCTGCAAA | ATAGCGATAT | CGTTACGCTT | 600 |
| CATGTGCCGC | TCAATACGGA | TACGCACTAT | ATTATCAGCC | ACGAACAAAT | 650 |
| ACAGAGAATG | AAGCAAGGAG | CATTTCTTAT | CAATACTGGG | CGCGGTCCAC | 700 |
| TTGTAGATAC | CTATGAGTTG | GTTAAAGCAT | TAGAAAACGG | GAAACTGGGC | 750 |
| GGTGCCGCAT | TGGATGTATT | GGAAGGAGAG | GAAGAGTTTT | TCTACTCTGA | 800 |
| TTGCACCCAA | AAACCAATTG | ATAATCAATT | TTTACTTAAA | CTTCAAAGAA | 850 |
| TGCCTAACGT | GATAATCACA | CCGCATACGG | CCTATTATAC | CGAGCAAGCG | 900 |
| TTGCGTGATA | CCGTTGAAAA | AACCATTAAA | AACTGTTTGG | ATTTTGAAAG | 950 |
| GAGACAGGAG | CATGAATAGA | ATAAAAGTTG | CAATACTGTT | TGGGGGTTGC | 1000 |
| TCAGAGGAGC | ATGACGTATC | GGTAAAATCT | GCAATAGAGA | TAGCCGCTAA | 1050 |
| CATTAATAAA | GAAAAATACG | AGCCGTTATA | CATTGGAATT | ACGAAATCTG | 1100 |
| GTGTATGGAA | AATGTGCGAA | AAACCTTGCG | CGGAATGGGA | AAACGACAAT | 1150 |
| TGCTATTCAG | CTGTACTCTC | GCCGGATAAA | AAAATGCACG | GATTACTTGT | 1200 |
| TAAAAAGAAC | CATGAATATG | AAATCAACCA | TGTTGATGTA | GCATTTTCAG | 1250 |
| CTTTGCATGG | CAAGTCAGGT | GAAGATGGAT | CCATACAAGG | TCTGTTTGAA | 1300 |
| TTGTCCGGTA | TCCCTTTTGT | AGGCTGCGAT | ATTCAAAGCT | CAGCAATTTG | 1350 |
| TATGGACAAA | TCGTTGACAT | ACATCGTTGC | GAAAAATGCT | GGGATAGCTA | 1400 |
| CTCCCGCCTT | TTGGGTTATT | AATAAAGATG | ATAGGCCGGT | GGCAGCTACG | 1450 |
| TTTACCTATC | CTGTTTTTGT | TAAGCCGGCG | CGTTCAGGCT | CATCCTTCGG | 1500 |
| TGTGAAAAAA | GTCAATAGCG | CGGACGAATT | GGACTACGCA | ATTGAATCGG | 1550 |
| CAAGACAATA | TGACAGCAAA | ATCTTAATTG | AGCAGGCTGT | TTCGGGCTGT | 1600 |
| GAGGTCGGTT | GTGCGGTATT | GGGAAACAGT | GCCGCGTTAG | TTGTTGGCGA | 1650 |
| GGTGGACCAA | ATCAGGCTGC | AGTACGGAAT | CTTTCGTATT | CATCAGGAAG | 1700 |
| TCGAGCCGGA | AAAAGGCTCT | GAAAACGCAG | TTATAACCGT | TCCCGCAGAC | 1750 |
| CTTTCAGCAG | AGGAGCGAGG | ACGGATACAG | GAAACGGCAA | AAAAAATATA | 1800 |
| TAAAGCGCTC | GGCTGTAGAG | GTCTAGCCCG | TGTGGATATG | TTTTTACAAG | 1850 |
| ATAACGGCCG | CATTGTACTG | AACGAAGTCA | ATACTCTGCC | CGGTTTCACG | 1900 |
| TCATACAGTC | GTTATCCCCG | TATGATGGCC | GCTGCAGGTA | TTGCACTTCC | 1950 |
| CGAACTGATT | GACCGCTTGA | TCGTATTAGC | GTTAAAGGGG | TGATAAGCAT | 2000 |
| GGAAATAGGA | TTTACTTTTT | TAGATGAAAT | AGTACACGGT | GTTCGTTGGG | 2050 |

SUBSTITUTE SHEET

147

| | | | | | |
|------------|------------|------------|------------|------------|------|
| ACGCTAAATA | TGCCACTTGG | GATAATTTCA | CCGGAAAACC | GGTTGACGGT | 2100 |
| TATGAAGTAA | ATCGCATTGT | AGGGACATAC | GAGTTGGCTG | AATCGCTTTT | 2150 |
| GAAGGCCAAA | GAAGTGGCTG | CTACCCAAGG | GTACGGATTG | CTTCTATGGG | 2200 |
| ACGGTTACCG | TCCTAAGCGT | GCTGTAAACT | GTTTTATGCA | ATGGGCTGCA | 2250 |
| CAGCCGGA | ATAACCTGAC | AAAGGAAAGT | TATTATCCCA | ATATTGACCG | 2300 |
| AACTGAGATG | ATTTCAAAAG | GATACGTGGC | TTCAAAATCA | AGCCATAGCC | 2350 |
| GCGGCAGTGC | CATTGATCTT | ACGCTTTATC | GATTAGACAC | GGGTGAGCTT | 2400 |
| GTACCAATGG | GGAGCCGATT | TGATTTTATG | GATGAACGCT | CTCATCATGC | 2450 |
| GGCAAATGGA | ATATCATGCA | ATGAAGCGCA | AAATCGCAGA | CGTTTGCGCT | 2500 |
| CCATCATGGA | AAACAGTGGG | TTTGAAGCAT | ATAGCCTCGA | ATGGTGGCAC | 2550 |
| TATGTATTAA | GAGACGAACC | ATACCCCAAT | AGCTATTTTG | ATTTCCCCGT | 2600 |
| TAAATAA | | | | | 2607 |

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1288 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

| | | | | | |
|------------|-------------|-------------|------------|------------|-----|
| GGATCCATCA | GGCAACGACG | GGCTGCTGCC | GGCCATCAGC | GGACGCAGGG | 50 |
| AGGACTTTCC | GCAACCGGCC | GTTTCGATGCG | GCACCGATGG | CCTTCGCGCA | 100 |
| GGGGTAGTGA | ATCCGCCAGG | ATTGACTTGC | GCTGCCCTAC | CTCTCACTAG | 150 |
| TGAGGGGCGG | CAGCGCATCA | AGCGGTGAGC | GCACTCCGGC | ACCGCCAACT | 200 |
| TTCAGCACAT | GCGTGTAAT | CATCGTCGTA | GAGACGTCGG | AATGGCCGAG | 250 |
| CAGATCCTGC | ACGGTTTCGAA | TGTCGTAACC | GCTGCGGAGC | AAGGCCGTCG | 300 |
| CGAACGAGTG | GCGGAGGGTG | TGCGGTGTGG | CGGGCTTCGT | GATGCCTGCT | 350 |
| TGTTCTACGG | CACGTTTGAA | GGCGCGCTGA | AAGGTCTGGT | CATACATGTG | 400 |
| ATGGCGACGC | ACGACACCGC | TCCGTGGATC | GGTCGAATGC | GTGTGCTGCG | 450 |
| CAAAAACCCA | GAACCACGGC | CAGGAATGCC | CGGCGCGCGG | ATACTTCCGC | 500 |
| TCAAGGGCGT | CGGGAAGCGC | AACGCCGCTG | CGGCCCTCGG | CCTGGTCCTT | 550 |
| CAGCCACCAT | GCCCGTGAC | GCGACAGCTG | CTCGCGCAGG | CTGGGTGCCA | 600 |
| AGCTCTCGGG | TAACATCAAG | GCCCCGATCCT | TGGAGCCCTT | GCCCTCCCGC | 650 |
| ACGATGATCG | TGCCGTGATC | GAAATCCAGA | TCCTTGACCC | GCAGTTGCAA | 700 |
| ACCCTCACTG | ATCCGCATGC | CCGTTCCATA | CAGAAGCTGG | GCGAACAAAC | 750 |
| GATGCTCGCC | TTCCAGAAAA | CCGAGGATGC | GAACCACTTC | ATCCGGGGTC | 800 |
| AGCACCACCG | GCAAGCGGCG | CTTCGCTGCA | CTTCCTGAAG | | 850 |

SUBSTITUTE SHEET

148

| | | | | | |
|------------|------------|------------|------------|-------------|------|
| CCAGGGCAGA | TCCGTGCACA | GCACCTTGCC | GTAGAAGAAC | AGCAAGGCCG | 900 |
| CCAATGCCTG | ACGATGCGTG | GAGACCGAAA | CCTTGCGCTC | GTTCGCCAGC | 950 |
| CAGGACAGAA | ATGCCTCGAC | TTCGCTGCTG | CCCAAGGTTG | CCGGGTGACG | 1000 |
| CACACCGTGG | AAACGGATGA | AGGCACGAAC | CCAGTGGACA | TAAGCCTGTT | 1050 |
| CGGTTCGTAA | GCTGTAATGC | AAGTAGCGTA | TGCGCTCACG | CAACTGGTCC | 1100 |
| AGAACCTTGA | CCGAACGCAG | CGGTGGTAAC | GGCGCAGTGG | CGGTTTTTCAT | 1150 |
| GGCTTGTTAT | GACTGTTTTT | TTGTACAGTC | TATGCCTCGG | GCATCCAAGC | 1200 |
| AGCAAGCGCG | TTACGCCGTG | GGTCGATGTT | TGATGTTATG | GAGCAGCAAC | 1250 |
| GATGTTACGC | AGCAGGGCAG | TCGCCCTAAA | ACAAAGTT | | 1288 |

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1650 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

| | | | | | |
|------------|------------|------------|------------|------------|------|
| GTTAGATGCA | CTAAGCACAT | AATTGCTCAC | AGCCAAACTA | TCAGGTCAAG | 50 |
| TCTGCTTTTA | TTATTTTAA | GCGTGCATAA | TAAGCCCTAC | ACAAATTGGG | 100 |
| AGATATATCA | TGAAAGGCTG | GCTTTTTCTT | GTTATCGCAA | TAGTTGGCGA | 150 |
| AGTAATCGCA | ACATCCGCAT | TAAAATCTAG | CGAGGGCTTT | ACTAAGCTTG | 200 |
| CCCCTTCCGC | CGTTGTCATA | ATCGGTTATG | GCATCGCATT | TTATTTTCTT | 250 |
| TCTCTGGTTC | TGAAATCCAT | CCCTGTCGGT | GTTGCTTATG | CAGTCTGGTC | 300 |
| GGGACTCGGC | GTCGTCATAA | TTACAGCCAT | TGCCTGGTTG | CTTCATGGGC | 350 |
| AAAAGCTTGA | TGCGTGGGGC | TTTGTAGGTA | TGGGGCTCAT | AATTGCTGCC | 400 |
| TTTTTGCTCG | CCCGATCCCC | ATCGTGGAAG | TCGCTGCGGA | GGCCGACGCC | 450 |
| ATGGTGACGG | TGTTCCGCAT | TCTGAATCTC | ACCGAGGACT | CCTTCTTCGA | 500 |
| TGAGAGCCGG | CGGCTAGACC | CCGCCGGCGC | TGTCACCGCG | GCGATCGAAA | 550 |
| TGCTGCGAGT | CGGATCAGAC | GTCGTGGATG | TCGGACCGGC | CGCCAGCCAT | 600 |
| CCGGACGCGA | GGCCTGTATC | GCCGGCCGAT | GAGATCAGAC | GTATTGCGCC | 650 |
| GCTCTTAGAC | GCCCTGTCCG | ATCAGATGCA | CCGTGTTTCA | ATCGACAGCT | 700 |
| TCCAACCGGA | AACCCAGCGC | TATGCGCTCA | AGCGCGGCGT | GGGCTACCTG | 750 |
| AACGATATCC | AAGGATTTCC | TGACCCTGCG | CTCTATCCCG | ATATTGCTGA | 800 |
| GGCGGACTGC | AGGCTGGTGG | TTATGCACTC | AGCGCAGCGG | GATGGCATCG | 850 |
| CCACCCGCAC | CGGTCACCTT | CGACCCGAAG | ACGCGCTCGA | CGAGATTGTG | 900 |
| CGGTTCTTCG | AGGCGCGGGT | TTCCGCCTTG | CGACGGAGCG | GGGTCGCTGC | 950 |
| CGACCGGCTC | ATCCTCGATC | CGGGGATGGG | ATTTTCTTG | AGCCCCGCAC | 1000 |

SUBSTITUTE SHEET

149

| | | | | | |
|------------|------------|-------------|------------|-------------|------|
| CGGAAACATC | GCTGCACGTG | CTGTGCAACC | TTCAAAAGCT | GAAGTCGGCG | 1050 |
| TTGGGGCTTC | CGCTATTGGT | CTCGGTGTCG | CGGAAATCCT | TCTTGGGCGC | 1100 |
| CACCGTTGGC | CTTCCTGTAA | AGGATCTGGG | TCCAGCGAGC | CTTGCGGCGG | 1150 |
| AACTTCACGC | GATCGGCAAT | GGCGCTGACT | ACGTCCGCAC | CCACGCGCCT | 1200 |
| GGAGATCTGC | GAAGCGCAAT | CACCTTCTCG | GAAACCCTCG | CGAAATTTTCG | 1250 |
| CAGTCGCGAC | GCCAGAGACC | GAGGGTTAGA | TCATGCCTAG | CATTACACCTT | 1300 |
| CCGGCCGCC | GCTAGCGGAC | CCTGGTCAGG | TTCCGCGAAG | GTGGGCGCAG | 1350 |
| ACATGCTGGG | CTCGTCAGGA | TCAAAC TGCA | CTATGAGGCG | GCGGTTTCATA | 1400 |
| CCGCGCCAGG | GGAGCGAATG | GACAGCGAGG | AGCCTCCGAA | CGTTCGGGTC | 1450 |
| GCCTGCTCGG | GTGATATCGA | CGAGGTTGTG | CGGCTGATGC | ACGACGCTGC | 1500 |
| GGCGTGATG | TCCGCCAAGG | GAACGCCCCG | CTGGGACGTC | GCGCGGATCG | 1550 |
| ACCGGACATT | CGCGGAGACC | TTCGTCCTGA | GATCCGAGCT | CCTAGTCGCG | 1600 |
| AGTTGCAGCG | ACGGCATCGT | CGGCTGTTGC | ACCTTGTCGG | CCGAGGATCC | 1650 |

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 630 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

| | | | | | |
|------------|------------|------------|------------|-------------|-----|
| ATGGGTCCGA | ATCCTATGAA | AATGTATCCT | ATAGAAGGAA | ACAAATCAGT | 50 |
| ACAATTTATC | AAACCTATTT | TAGAAAAATT | AGAAAATGTT | GAGGTTGGAG | 100 |
| AATACTCATA | TTATGATTCT | AAGAATGGAG | AACTTTTGA | TAAGCAAATT | 150 |
| TTATATCATT | ATCCAATCTT | AAACGATAAG | TTAAAAATAG | GTAAATTTTG | 200 |
| CTCAATAGGA | CCAGGTGTAA | CTATTATTAT | GAATGGAGCA | AATCATAGAA | 250 |
| TGGATGGCTC | AACATATCCA | TTTAATTTAT | TTGGTAATGG | ATGGGAGAAA | 300 |
| CATATGCCAA | AATTAGATCA | ACTACCTATT | AAGGGGGATA | CAATAATAGG | 350 |
| TAATGATGTA | TGGATAGGAA | AAGATGTTGT | AATTATGCCA | GGAGTAAAAA | 400 |
| TCGGGGATGG | TGCAATAGTA | GCTGCTAATT | CTGTTGTTGT | AAAAGATATA | 450 |
| GCGCCATACA | TGTTAGCTGG | AGGAAATCCT | GCTAACGAAA | TAAAACAAAG | 500 |
| ATTTGATCAA | GATACAATAA | ATCAGCTGCT | TGATATAAAA | TGGTGGGAATT | 550 |
| GGCCAATAGA | CATTATTAAT | GAGAATATAG | ATAAAATTCT | TGATAATAGC | 600 |
| ATCATTAGAG | AAGTCATATG | GAAAAAATGA | | | 630 |

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET

150

- (A) LENGTH: 1440 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

| | | | | | |
|-------------|-------------|-------------|------------|------------|------|
| ATGAATATAG | TTGAAAATGA | AATATGTATA | AGAACTTTAA | TAGATGATGA | 50 |
| TTTTCCTTTG | ATGTTAAAAT | GGTTAACTGA | TGAAAGAGTA | TTAGAATTTT | 100 |
| ATGGTGGTAG | AGATAAAAAA | TATACATTAG | AATCATTTAA | AAAACATTAT | 150 |
| ACAGAGCCTT | GGGAAGATGA | AGTTTTTAGA | GTAATTATTG | AATATAACAA | 200 |
| TGTTCCCTATT | GGATATGGAC | AAATATATAA | AATGTATGAT | GAGTTATATA | 250 |
| CTGATTATCA | TTATCCAAAA | ACTGATGAGA | TAGTCTATGG | TATGGATCAA | 300 |
| TTTATAGGAG | AGCCAAATTA | TTGGAGTAAA | GGAATTGGTA | CAAGATATAT | 350 |
| TAAATTGATT | TTTGAATTTT | TGAAAAAAGA | AAGAAATGCT | AATGCAGTTA | 400 |
| TTTTAGACCC | TCATAAAAAAT | AATCCAAGAG | CAATAAGGGC | ATACCAAAAA | 450 |
| TCTGGTTTTA | GAATTATTGA | AGATTTGCCA | GAACATGAAT | TACACGAGGG | 500 |
| CAAAAAAGAA | GATTGTTATT | TAATGGAATA | TAGATATGAT | GATAATGCCA | 550 |
| CAAATGT TAA | GGCAATGAAA | TATTTAATTG | AGCATTACTT | TGATAATTTT | 600 |
| AAAGTAGATA | GTATTGAAAT | AATCGGTAGT | GGTTATGATA | GTGTGGCATA | 650 |
| TTTAGTTAAT | AATGAATACA | TTTTTAAAC | AAAATTTAGT | ACTAATAAGA | 700 |
| AAAAAGGTTA | TGCAAAAGAA | AAAGCAATAT | ATAATTTTTT | AAATACAAAT | 750 |
| TTAGAAACTA | ATGTAAAAAT | TCCTAATATT | GAATATTCGT | ATATTAGTGA | 800 |
| TGAATTATCT | ATACTAGGTT | ATAAAGAAAT | TAAAGGAACT | TTTTTAACAC | 850 |
| CAGAAATTTA | TTCTACTATG | TCAGAAGAAG | AACAAAATTT | GTTAAAACGA | 900 |
| GATATTGCCA | GTTTTTTAAG | ACAAATGCAC | GGTTTAGATT | ATACAGATAT | 950 |
| TAGTGAATGT | ACTATTGATA | ATAAACAAAA | TGTATTAGAA | GAGTATATAT | 1000 |
| TGTTGCGTGA | AACTATTTAT | AATGATTTAA | CTGATATAGA | AAAAGATTAT | 1050 |
| ATAGAAAGTT | TTATGGAAAAG | ACTAAATGCA | ACAACAGTTT | TTGAGGGTAA | 1100 |
| AAAGTGTTTA | TGCCATAATG | ATTTTtagTTG | TAATCATCTA | TTGTTAGATG | 1150 |
| GCAATAATAG | ATTAAGTGA | ATAATTGATT | TTGGAGATTC | TGGAATTATA | 1200 |
| GATGAATATT | GTGATTTTAT | ATACTTACTT | GAAGATAGTG | AAGAAGAAAT | 1250 |
| AGGAACAAAT | TTTGGAGAAG | ATATATTAAG | AATGTATGGA | AATATAGATA | 1300 |
| TTGAGAAAGC | AAAAGAATAT | CAAGATATAG | TTGAAGAATA | TTATCCTATT | 1350 |
| GAAACTATTG | TTTATGGAAT | TAAAAATATT | AAACAGGAAT | TTATCGAAAA | 1400 |
| TGGTAGAAAA | GAAATTTATA | AAAGGACTTA | TAAAGATTGA | | 1440 |

(2) INFORMATION FOR SEQ ID NO: 175:

SUBSTITUTE SHEET

457

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

| | | | | | |
|--------------|-------------|------------|------------|------------|-----|
| TTGAATTTAA | ACAATGACCA | TGGACCTGAT | CCCGAAAATA | TTTTACCGAT | 50 |
| AAAAGGGAAT | CGGAATCTTC | AATTTATAAA | ACCTACTATA | ACGAACGAAA | 100 |
| ACATTTTGGT | GGGGAATAT | TCTTATTATG | ATAGTAAGCG | AGGAGAATCC | 150 |
| TTTGAAGATC | AAGTCTTATA | TCATTATGAA | GTGATTGGAG | ATAAGTTGAT | 200 |
| TATAGGAAGA | TTTGTGTTCAA | TTGGTCCCGG | AACAACATTT | ATTATGAATG | 250 |
| GTGCAAACCA | TCGGATGGAT | GGATCAACAT | ATCCTTTTCA | TCTATTCAGG | 300 |
| ATGGGTGTTGGG | AGAAGTATAT | GCCTTCCTTA | AAAGATCTTC | CCTTGAAAGG | 350 |
| GGACATTGAA | ATTGGAAATG | ATGTATGGAT | AGGTAGAGAT | GTAACCATTA | 400 |
| TGCCTGGGGT | GAAAATTGGG | GACGGGGCAA | TCATTGCTGC | AGAAGCTGTT | 450 |
| GTCACAAAGA | ATGTTGCTCC | CTATTCTATT | GTGGGTGGAA | ATCCCTTAAA | 500 |
| ATTTATAAGA | AAAAGGTTTT | CTGATGGAGT | TATCGAAGAA | TGGTTAGCTT | 550 |
| TACAATGGTG | GAATTTAGAT | ATGAAAATTA | TTAATGAAAA | TCTTCCCTTC | 600 |
| ATAATAAATG | GAGATATCGA | AATGCTGAAG | AGAAAAAGAA | AACTTCTAGA | 650 |
| TGACACTTGA | | | | | 660 |

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1569 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

| | | | | | |
|------------|------------|------------|-------------|------------|-----|
| ATGAAAATAA | TGTTAGAGGG | ACTTAATATA | AAACATTATG | TTCAAGATCG | 50 |
| TTTATTGTTG | AACATAAATC | GCCTAAAGAT | TTATCAGAA | GATCGTATTG | 100 |
| GTTTAATTGG | TAAAAATGGA | AGTGGAAAAA | CAACGTTACT | TCACATATTA | 150 |
| TATAAAAAAA | TTGTGCCTGA | AGAAGGTATT | GTAAAAACAAT | TTTCACATTG | 200 |
| TGAACTTATT | CCTCAATTGA | AGCTCATAGA | ATCAACTAAA | AGTGGTGGTG | 250 |
| AAGTAACACG | AAACTATATT | CGGCAAGCGC | TTGATAAAAA | TCCAGAACTG | 300 |
| CTATTAGCAG | ATGAACCAAC | AAGTAAATTA | GAAAAAAGC | TTTAGAAAAA | 350 |

SUBSTITUTE SHEET

152

| | | | | | |
|------------|------------|-------------|------------|------------|------|
| ATTAGAACAG | GATTTAAAAA | ATTGGCATGG | AGCATTATT | ATAGTTTCAC | 400 |
| ATGATCGCGC | TTTTTTAGAT | AACTTGTGTA | CTACTATATG | GGAAATTGAC | 450 |
| GAGGGAAGAA | TAACTGAATA | TAAGGGGAAT | TATAGTAACT | ATGTTGAACA | 500 |
| AAAAGAATTA | GAAAGACATC | GAGAAGAATT | AGAATATGAA | AAATATGAAA | 550 |
| AAGAAAAGAA | ACGATTGGAA | AAAGCTATAA | ATATAAAAGA | ACAGAAAGCT | 600 |
| CAACGAGCAA | CTAAAAAACC | GAAAAACTTA | AGTTTATCTG | AAGGCAAAAT | 650 |
| AAAAGGAGCA | AAGCCATACT | TTGCAGGTAA | GCAAAAGAAG | TTACGAAAAA | 700 |
| CTGTAAAATC | TCTAGAAACC | AGACTAGAAA | AACTTGAAAG | CGTCGAAAAG | 750 |
| AGAAACGAAC | TTCCTCCACT | TAAAATGGAT | TTAGTGAAGT | TAGAAAGTGT | 800 |
| AAAAAATAGA | ACTATAATAC | GTGGTGAAGA | TGTCTCGGGT | ACAATTGAAG | 850 |
| GACGGGTATT | GTGGAAAGCA | AAAAGTTTTA | GTATTCGCGG | AGGAGACAAG | 900 |
| ATGGCAATTA | TCGGATCTAA | TGGTACAGGA | AAGACAACGT | TTATTAAAAA | 950 |
| AATTGTGCAT | GGAATCCTG | GTATTTTCATT | ATCGCCATCT | GTCAAAATCG | 1000 |
| GTTATTTTAG | CCAAAAAATA | GATACATTAG | AATTAGATAA | GAGCATTTTA | 1050 |
| GAAAATGTTT | AATCTTCTTC | ACAACAAAAT | GAAACTCTTA | TTCGAACTAT | 1100 |
| TCTAGCTAGA | ATGCATTTTT | TTAGAGATGA | TGTTTATAAA | CCAATAAGTG | 1150 |
| TCTTAAGTGG | TGGAGAGCGA | GTTAAAGTAG | CACTAACTAA | AGTATTCTTA | 1200 |
| AGTGAAGTTA | ATACGTTGGT | ACTAGATGAA | CCAACAACT | TTCTTGATAT | 1250 |
| GGAAGCTATA | GAGGCGTTTG | AATCTTTGTT | AAAGGAATAT | AATGGCAGTA | 1300 |
| TAATCTTTGT | ATCTCACGAT | CGTAAATTTA | TCGAAAAAGT | AGCCACTCGA | 1350 |
| ATAATGACAA | TTGATAATAA | AGAAATAAAA | ATATTTGATG | GCACATATGA | 1400 |
| ACAATTTAAA | CAAGCTGAAA | AGCCAACAAG | GAATATTAAA | GAAGATAAAA | 1450 |
| AACTTTTACT | TGAGACAAAA | ATTACAGAAG | TACTCAGTCG | ATTGAGTATT | 1500 |
| GAACCTTCGG | AAGAATTAGA | ACAAGAGTTT | CAAACTTAA | TAAATGAAAA | 1550 |
| AAGAAATTTG | GATAAATAA | | | | 1569 |

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1467 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATGGAACAAT | ATACAATTAA | ATTTAACCAA | ATCAATCATA | AATTGACAGA | 50 |
| TTTACGATCA | CTTAACATCG | ATCATCTTTA | TGCTTACCAA | TTTGAAAAAA | 100 |

SUBSTITUTE SHEET

153

| | | | | | |
|------------|------------|-------------|------------|------------|------|
| TAGCACTTAT | TGGGGGTAAT | GGTACTGGTA | AAACCACATT | ACTAAATATG | 150 |
| ATTGCTCAAA | AAACAAAACC | AGAATCTGGA | ACAGTTGAAA | CGAATGGCGA | 200 |
| AATTCAATAT | TTTGAACAGC | TTAACATGGA | TGTGGAAAAT | GATTTTAAAC | 250 |
| CGTTAGACGG | TAGTTTAATG | AGTGAACTCC | ATATACCTAT | GCATACAACC | 300 |
| GACAGTATGA | GTGGTGGTGA | AAAAGCAAAA | TATAAATTAC | GTAATGTCAT | 350 |
| ATCAAATTAT | AGTCCGATAT | TACTTTTAGA | TGAACCTACA | AATCACTTGG | 400 |
| ATAAAATTGG | TAAAGATTAT | CTGAATAATA | TTTTAAAATA | TTACTATGGT | 450 |
| ACTTTAATTA | TAGTAAGTCA | CGATAGAGCA | CTTATAGACC | AAATTGCTGA | 500 |
| CACAATTTGG | GATATACAAG | AAGATGGCAC | AATAAGAGTG | TTTAAAGGTA | 550 |
| ATTACACACA | GTATCAAAAT | CAATATGAAC | AAGAACAGTT | AGAACAACAA | 600 |
| CGTAAATATG | AACAGTATAT | AAGTGAAAAA | CAAAGATTGT | CCCAAGCCAG | 650 |
| TAAAGCTAAA | CGAAATCAAG | CGCAACAAAT | GGCACAAGCA | TCATCAAAAC | 700 |
| AAAAAAATAA | AAGTATAGCA | CCAGATCGTT | TAAGTGCATC | AAAAGAAAAA | 750 |
| GGCACGGTTG | AGAAGGCTGC | TCAAAAACAA | GCTAAGCATA | TTGAAAAAAG | 800 |
| AATGGAACAT | TTGGAAGAAG | TTGAAAAACC | ACAAAGTTAT | CATGAATTCA | 850 |
| ATTTTCCACA | AAATAAAATT | TATGATATCC | ATAATAATTA | TCCAATCATT | 900 |
| GCACAAAATC | TAACATTGGT | TAAAGGAAGT | CAAAAACTGC | TAACACAAGT | 950 |
| ACGATTCCAA | ATACCATATG | GCAAAAATAT | AGCGCTCGTA | GGTGCAAATG | 1000 |
| GTGTAGGTAA | GACAACTTTA | CTTGAAGCTA | TTTACCACCA | AATAGAGGGA | 1050 |
| ATTGATTGTT | CTCCTAAAGT | GCAAAATGGCA | TACTATCGTC | AACTTGCTTA | 1100 |
| TGAAGACATG | CGTGACGTTT | CATTATTGCA | ATATTTAATG | GATGAAACGG | 1150 |
| ATTCATCAGA | ATCATTCAGT | AGAGCTATTT | TAAATAACTT | GGGTTTAAAT | 1200 |
| GAAGCACTTG | AGCGTTCCTG | TAATGTTTTG | AGTGGTGGGG | AAAGAACGAA | 1250 |
| ATTATCGTTA | GCAGTATTAT | TTTCAACGAA | AGCGAATATG | TTAATTTTGG | 1300 |
| ATGAACCAAC | TAATTTTTTA | GATATTAAAA | CATTAGAAGC | ATTAGAAATG | 1350 |
| TTTATGAATA | AATATCCTGG | AATCATTTTG | TTTACATCAC | ATGATACAAG | 1400 |
| GTTTGTTAAA | CATGTATCAG | ATAAAAAATG | GGAATTAACA | GGACAATCTA | 1450 |
| TTCATGATAT | AACTTAA | | | | 1467 |

SUBSTITUTE SHEET

154

CLAIMS**What is claimed is:**

1. A method using probes (fragments and/or oligonucleotides)
5 and/or amplification primers which are specific, ubiquitous
and sensitive for determining the presence and/or amount of
nucleic acids from bacterial species selected from the group
consisting of *Escherichia coli*, *Klebsiella pneumoniae*,
10 *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus*
pneumoniae, *Staphylococcus aureus*, *Staphylococcus epidermidis*,
Enterococcus faecalis, *Staphylococcus saprophyticus*,
Streptococcus pyogenes, *Haemophilus influenzae* and *Moraxella*
catarrhalis in a any sample suspected of containing said
15 bacterial nucleic acid, wherein said bacterial nucleic acid or
variant or part thereof comprises a selected target region
hybridizable with said probes or primers; said method
comprising the steps of contacting said sample with said
probes or primers and detecting the presence and/or amount of
20 hybridized probes and/or amplified products as an indication
of the presence and/or amount of said bacterial species.
2. A method as defined in claim 1 further using probes
(fragments and/or oligonucleotides) and/or amplification
25 primers which are universal and sensitive for determining the
presence and/or amount of nucleic acids from any bacteria from
any sample suspected of containing said bacterial nucleic
acid, wherein said bacterial nucleic acid or variant or part
thereof comprises a selected target region hybridizable with
said probes or primers; said method comprising the steps of
30 contacting said sample with said probes or primers and
detecting the presence and/or amount of hybridized probes
and/or amplified products as an indication of the presence
and/or amount of said any bacteria.
- 35 3. A method as defined in claim 1 further using probes
(fragments and/or oligonucleotides) and/or amplification
primers which are sp cific, ubiquitous and sensitive for

SUBSTITUTE SHEET

155

- determining the presence and/or amount of nucleic acids from an antibiotic resistance gene selected from the group consisting of *bla_{tem}*, *Blarob*, *Blashv*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *mecA*, *vanA*, *vanH*, *vanX*, *satA*, *aacA-aphD*, *vat*,
5 *vga*, *msrA*, *sul* and *int* in any sample suspected of containing said bacterial nucleic acid, wherein said bacterial nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers; said method comprising the steps of contacting said sample with said
10 probes or primers and detecting the presence and/or amount of hybridized probes and/or amplified products as an indication of the presence and/or amount of said antibiotic resistance gene.
- 15 4. The method of any one of claims 1, 2 and 3 which is performed directly on a sample obtained from human patients, animals, environment or food.
- 20 5. The method of any one of claims 1, 2 and 3 which is performed directly on a sample consisting of one or more bacterial colonies.
- 25 6. The method of any one of claims 1 to 5, wherein the bacterial nucleic acid is amplified by a method selected from the group consisting of:
- a) polymerase chain reaction (PCR),
 - b) ligase chain reaction,
 - c) nucleic acid sequence-based amplification,
 - d) self-sustained sequence replication,
 - 30 e) strand displacement amplification,
 - f) branched DNA signal amplification,
 - g) nested PCR, and
 - h) multiplex PCR.
- 35 7. The method of claim 6 wherein said bacterial nucleic acid is amplified by PCR.

SUBSTITUTE SHEET

186

8. The method of claim 7 wherein the PCR protocol is modified to determine within one hour the presence of said bacterial nucleic acids by performing for each amplification cycle an annealing step of only one second at 55°C and a
5 denaturation step of only one second at 95°C without any elongation step.

9. A method for the detection, identification and/or quantification of *Escherichia coli* directly from a test sample
10 or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from
15 this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

20 said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group
25 consisting of SEQ ID NO:3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Escherichia coli*, under conditions such that the nucleic acid
30 of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present n a first reactive member of said labelling means, said first reactiv member
35 reacting with a second reactive member present on said probe; and

SUBSTITUTE SHEET

157

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Escherichia coli* in said test sample.

5

10. A method as defined in claim 9, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-227 nucleotides in length which sequence is comprised in SEQ ID NO: 3 or a complementary sequence thereof,

2) an oligonucleotide of 12-278 nucleotides in length which sequence is comprised in SEQ ID NO: 4 or a complementary sequence thereof,

3) an oligonucleotide of 12-1596 nucleotides in length which sequence is comprised in SEQ ID NO: 5 or a complementary sequence thereof,

4) an oligonucleotide of 12-2703 nucleotides in length which sequence is comprised in SEQ ID NO: 6 or a complementary sequence thereof,

5) an oligonucleotide of 12-1391 nucleotides in length which sequence is comprised in SEQ ID NO: 7 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Escherichia coli*.

25

11. The method of claim 10, wherein the probe for detecting nucleic acid sequences from *Escherichia coli* is selected from the group consisting of SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54 and a sequence complementary thereof.

35

12. A method for detecting the presence and/or amount of *Escherichia coli* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having

SUBSTITUTE SHEET

158

at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Escherichia coli* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6 and SEQ ID NO: 7;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Escherichia coli* in said test sample.

13. The method of claim 12, wherein said at least one pair of primers is selected from the group consisting of:

- a) SEQ ID NO: 42 and SEQ ID NO: 43,
- b) SEQ ID NO: 46 and SEQ ID NO: 47,
- c) SEQ ID NO: 55 and SEQ ID NO: 56, and
- d) SEQ ID NO: 131 and SEQ ID NO: 132.

14. A method for the detection, identification and/or quantification of *Klebsiella pneumoniae* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

SUBSTITUTE SHEET

159

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO:8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Klebsiella pneumoniae*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Klebsiella pneumoniae* in said test sample.

15. A method as defined in claim 14, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-238 nucleotides in length which sequence is comprised in SEQ ID NO: 8 or a complementary sequence thereof,

2) an oligonucleotide of 12-385 nucleotides in length which sequence is comprised in SEQ ID NO: 9 or a complementary sequence thereof,

3) an oligonucleotide of 12-462 nucleotides in length which sequence is comprised in SEQ ID NO: 10 or a complementary sequence thereof,

4) an oligonucleotide of 12-730 nucleotides in length which sequence is comprised in SEQ ID NO: 11 or a complementary sequence thereof, and

SUBSTITUTE SHEET

166

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Klebsiella pneumoniae*.

- 5 16. The method of claim 15, wherein the probe for detecting nucleic acid sequences from *Klebsiella pneumoniae* is selected from the group consisting of SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 69 and a sequence
10 complementary thereof.

17. A method for detecting the presence and/or amount of *Klebsiella pneumoniae* in a test sample which comprises the following steps:

- 15 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Klebsiella pneumoniae* DNA that
20 contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ
25 ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, and SEQ ID NO: 11;
- b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and
- 30 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Klebsiella pneumoniae* in said test sample.

18. The method of claim 17, wherein said at least one pair of
35 primers is selected from the group consisting of:

a) SEQ ID NO: 61 and SEQ ID NO: 62,

b) SEQ ID NO: 67 and SEQ ID NO: 68

SUBSTITUTE SHEET

161

- c) SEQ ID NO: 135 and SEQ ID NO: 136, and
- d) SEQ ID NO: 137 and SEQ ID NO: 138.

19. A method for the detection, identification and/or
5 quantification of *Proteus mirabilis* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving
in solution the bacterial DNA of the sample or of a
10 substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous
population of bacteria isolated from this sample on an inert
support, and lysing in situ said inoculated sample or isolated
15 bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single
stranded form;

b) contacting said single stranded DNA with a probe, said
probe comprising at least one single stranded nucleic acid
20 which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Proteus mirabilis*,
25 under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said
30 labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label
on said inert support or in said solution as an indication of
the presence and/or amount of *Proteus mirabilis* in said test
35 sample.

SUBSTITUTE SHEET

162

20. A method as defined in claim 19, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-225 nucleotides in length which sequence is comprised in SEQ ID NO: 12 or a
5 complementary sequence thereof,

2) an oligonucleotide of 12-402 nucleotides in length which sequence is comprised in SEQ ID NO: 13 or a complementary sequence thereof,

3) an oligonucleotide of 12-157 nucleotides in length
10 which sequence is comprised in SEQ ID NO: 14 or a complementary sequence thereof,

4) an oligonucleotide of 12-1348 nucleotides in length which sequence is comprised in SEQ ID NO: 15 or a complementary sequence thereof, and

15 variants thereof which specifically and ubiquitously anneal with strains and representatives of *Proteus mirabilis*.

21. The method of claim 20, wherein the probe for detecting nucleic acid sequences from *Proteus mirabilis* is selected from
20 the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82 and a sequence complementary thereof.

25 22. A method for detecting the presence and/or amount of *Proteus mirabilis* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having
30 at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Proteus mirabilis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an
35 extension product which contains the target sequence as a template, said at least one pair of primers being chosen from

SUBSTITUTE SHEET

163

within one of the following sequences: SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, and SEQ ID NO: 15;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Proteus mirabilis* in said test sample.

10

23. The method of claim 22, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 74 and SEQ ID NO: 75, and

b) SEQ ID NO: 133 and SEQ ID NO: 134.

15

24. A method for the detection, identification and/or quantification of *Staphylococcus saprophyticus* directly from a test sample or from bacterial colonies, which comprises the following steps:

20 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

25 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

30 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, a sequence complementary thereof, a part thereof
35 and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Staphylococcus saprophyticus*, under conditions such that the nucleic acid of

SUBSTITUTE SHEET

164

said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of
5 said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus saprophyticus* in
10 said test sample.

25. A method as defined in claim 24, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-172 nucleotides in length
15 which sequence is comprised in SEQ ID NO: 21 or a complementary sequence thereof,

2) an oligonucleotide of 12-155 nucleotides in length which sequence is comprised in SEQ ID NO: 22 or a complementary sequence thereof,

20 3) an oligonucleotide of 12-145 nucleotides in length which sequence is comprised in SEQ ID NO: 23 or a complementary sequence thereof,

4) an oligonucleotide of 12-265 nucleotides in length which sequence is comprised in SEQ ID NO: 24 or a
25 complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus saprophyticus*.

30 26. The method of claim 25, wherein the probe for detecting nucleic acid sequences from *Staphylococcus saprophyticus* is selected from the group consisting of SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104 and a sequence complementary thereof.

35

SUBSTITUTE SHEET

165

27. A method for detecting the presence and/or amount of *Staphylococcus saprophyticus* in a test sample which comprises the following steps:

5 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus saprophyticus* DNA that contains a target sequence, and the other of said primers
10 being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, and SEQ ID NO: 24;

15 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

20 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus saprophyticus* in said test sample.

28. The method of claim 27, wherein said at least one pair of primers is selected from the group consisting of:

- 25 a) SEQ ID NO: 98 and SEQ ID NO: 99, and
b) SEQ ID NO: 139 and SEQ ID NO: 140.

29. A method for the detection, identification and/or quantification of *Moraxella catarrhalis* directly from a test
30 sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving
in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from
35 this sample, or

inoculating said sampl or said substantially homogenous population of bacteria isolated from this sample on an inert

SUBSTITUTE SHEET

166

support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

- 5 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 28, SEQ ID NO: 29, a sequence complementary thereof, a part thereof and a variant thereof,
- 10 which specifically and ubiquitously anneals with strains or representatives of *Moraxella catarrhalis*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling
- 15 means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

- 20 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Moraxella catarrhalis* in said test sample.

30. A method as defined in claim 29, wherein said probe is
- 25 selected from the group consisting of:

- 1) an oligonucleotide of 12-526 nucleotides in length which sequence is comprised in SEQ ID NO: 28 or a complementary sequence thereof,
- 2) an oligonucleotide of 12-466 nucleotides in length
- 30 which sequence is comprised in SEQ ID NO: 29 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Moraxella catarrhalis*.

35

31. The method of claim 30, wherein the probe for detecting nucleic acid sequences from *Moraxella catarrhalis* is selected

SUBSTITUTE SHEET

167

from the group consisting of SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117 and a sequence complementary thereof.

5

32. A method for detecting the presence and/or amount of *Moraxella catarrhalis* in a test sample which comprises the following steps:

10 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Moraxella catarrhalis* DNA that contains a target sequence, and the other of said primers
15 being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 28 and SEQ ID NO: 29;

20 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

25 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Moraxella catarrhalis* in said test sample.

33. The method of claim 32, wherein said at least one pair of primers is selected from the group consisting of:

- 30 a) SEQ ID NO: 112 and SEQ ID NO: 113,
b) SEQ ID NO: 118 and SEQ ID NO: 119, and
c) SEQ ID NO: 160 and SEQ ID NO: 119.

34. A method for the detection, identification and/or
35 quantification of *Pseudomonas aeruginosa* directly from a test sample or from bacterial colonies, which comprises the following steps:

SUBSTITUTE SHEET

168

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

5 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single
10 stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ
15 ID NO: 19, SEQ ID NO: 20, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Pseudomonas aeruginosa*, under conditions such that the nucleic acid of said probe can selectively hybridize with said
20 bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said
25 probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Pseudomonas aeruginosa* in said test sample.

30

35. A method as defined in claim 34, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-2167 nucleotides in length which sequence is comprised in SEQ ID NO: 16 or a
35 complementary sequence thereof,

SUBSTITUTE SHEET

169

2) an oligonucleotide of 12-1872 nucleotides in length which sequence is comprised in SEQ ID NO: 17 or a complementary sequence thereof,

3) an oligonucleotide of 12-3451 nucleotides in length
5 which sequence is comprised in SEQ ID NO: 18 or a complementary sequence thereof,

4) an oligonucleotide of 12-744 nucleotides in length which sequence is comprised in SEQ ID NO: 19 or a complementary sequence thereof,

10 5) an oligonucleotide of 12-2760 nucleotides in length which sequence is comprised in SEQ ID NO: 20 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Pseudomonas*
15 *aeruginosa*.

36. The method of claim 35, wherein the probe for detecting nucleic acid sequences from *Pseudomonas aeruginosa* is selected from the group consisting of SEQ ID NO: 87, SEQ ID NO: 88, SEQ
20 ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95 and a sequence complementary thereof.

37. A method for detecting the presence and/or amount of
25 *Pseudomonas aeruginosa* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being
30 capable of hybridizing selectively with one of the two complementary strands of *Pseudomonas aeruginosa* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target
35 sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ

SUBSTITUTE SHEET

170

ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Pseudomonas aeruginosa* in said test sample.

10

38. The method of claim 37, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 83 and SEQ ID NO: 84, and

b) SEQ ID NO: 85 and SEQ ID NO: 86.

15

39. A method for the detection, identification and/or quantification of *Staphylococcus epidermidis* directly from a test sample or from bacterial colonies, which comprises the following steps:

20 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

25 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

30 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 36, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Staphylococcus epidermidis*, under conditions such that the nucleic acid of said probe can selectively hybridize with said

SUBSTITUTE SHEET

171

bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

5 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus epidermidis* in
10 said test sample.

40. A method as defined in claim 39, wherein said probe is selected from the group consisting of an oligonucleotide of 12-705 nucleotides in length which sequence is comprised in
15 SEQ ID NO: 36 and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus epidermidis*.

41. A method for detecting the presence and/or amount of
20 *Staphylococcus epidermidis* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being
25 capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus epidermidis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target
30 sequence as a template, said at least one pair of primers being chosen from within the following sequence: SEQ ID NO: 36;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence,
35 and amplifying said target sequence, if any, to a detectable level; and

SUBSTITUTE SHEET

179

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus epidermidis* in said test sample.

5 42. The method of claim 41, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 145 and SEQ ID NO: 146, and

b) SEQ ID NO: 147 and SEQ ID NO: 148.

10 43. A method for the detection, identification and/or quantification of *Staphylococcus aureus* directly from a test sample or from bacterial colonies, which comprises the following steps:

15 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

20 said bacterial DNA being in a substantially single stranded form;

25 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 37, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of
30 *Staphylococcus aureus*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by lab lling means, the label being present on said probe or the label being present on a first
35 reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

SUBSTITUTE SHEET

173

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus aureus* in said test sample.

5

44. A method as defined in claim 43, wherein said probe is selected from the group consisting of an oligonucleotide of 12-442 nucleotides in length which sequence is comprised in SEQ ID NO: 37 and variants thereof which specifically and
10 ubiquitously anneal with strains and representatives of *Staphylococcus aureus*.

45. A method for detecting the presence and/or amount of *Staphylococcus aureus* in a test sample which comprises the
15 following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two
20 complementary strands of *Staphylococcus aureus* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers
25 being chosen from within the following sequence: SEQ ID NO: 37;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable
30 level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus aureus* in said test sample.

35 46. The method of claim 45, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 149 and SEQ ID NO: 150,

SUBSTITUTE SHEET

174

- b) SEQ ID NO: 149 and SEQ ID NO: 151, and
c) SEQ ID NO: 152 and SEQ ID NO: 153.

47. A method for the detection, identification and/or
5 quantification of *Haemophilus influenzae* directly from a test
sample or from bacterial colonies, which comprises the
following steps:

a) depositing and fixing on an inert support or leaving
in solution the bacterial DNA of the sample or of a
10 substantially homogenous population of bacteria isolated from
this sample, or

inoculating said sample or said substantially homogenous
population of bacteria isolated from this sample on an inert
support, and lysing in situ said inoculated sample or isolated
15 bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single
stranded form;

b) contacting said single stranded DNA with a probe, said
probe comprising at least one single stranded nucleic acid
20 which nucleotidic sequence is selected from the group
consisting of SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, a
sequence complementary thereof, a part thereof and a variant
thereof, which specifically and ubiquitously anneals with
strains or representatives of *Haemophilus influenzae*, under
25 conditions such that the nucleic acid of said probe can
selectively hybridize with said bacterial DNA, whereby a
hybridization complex is formed, said complex being detected
by labelling means, the label being present on said probe or
the label being present on a first reactive member of said
30 labelling means, said first reactive member reacting with a
second reactive member present on said probe; and

c) detecting the presence or the intensity of said label
on said inert support or in said solution as an indication of
the presence and/or amount of *Haemophilus influenzae* in said
35 test sample.

SUBSTITUTE SHEET

175

48. A method as defined in claim 47, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-845 nucleotides in length which sequence is comprised in SEQ ID NO: 25 or a
5 complementary sequence thereof,

2) an oligonucleotide of 12-1598 nucleotides in length which sequence is comprised in SEQ ID NO: 26 or a complementary sequence thereof,

3) an oligonucleotide of 12-9100 nucleotides in length
10 which sequence is comprised in SEQ ID NO: 27 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Haemophilus influenzae*.

15

49. The method of claim 48, wherein the probe for detecting nucleic acid sequences from *Haemophilus influenzae* is selected from the group consisting of SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107 and a sequence complementary thereof.

20

50. A method for detecting the presence and/or amount of *Haemophilus influenzae* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution
25 containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Haemophilus influenzae* DNA that contains a target sequence, and the other of said primers
30 being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27;

35 b) synthesizing an extension product of each of said primers which extension products contain the target sequence,

SUBSTITUTE SHEET

176

and amplifying said target sequence, if any, to a detectable level; and

- c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Haemophilus influenzae* in said test sample.

51. The method of claim 50, wherein said at least one pair of primers comprises the following pair: SEQ ID NO: 154 and SEQ ID NO: 155.

10

52. A method for the detection, identification and/or quantification of *Streptococcus pneumoniae* directly from a test sample or from bacterial colonies, which comprises the following steps:

- 15 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

- 25 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 35, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Streptococcus pneumoniae*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being
- 30 detected by labelling means, the label being present on said probe or the label being present on a first reactive member of
- 35

SUBSTITUTE SHEET

177

said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

- c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Streptococcus pneumoniae* in said test sample.

53. A method as defined in claim 52, wherein said probe is selected from the group consisting of:

- 10 1) an oligonucleotide of 12-631 nucleotides in length which sequence is comprised in SEQ ID NO: 30 or a complementary sequence thereof,
- 2) an oligonucleotide of 12-3754 nucleotides in length which sequence is comprised in SEQ ID NO: 31 or a complementary sequence thereof,
- 15 3) an oligonucleotide of 12-841 nucleotides in length which sequence is comprised in SEQ ID NO: 34 or a complementary sequence thereof,
- 4) an oligonucleotide of 12-4500 nucleotides in length which sequence is comprised in SEQ ID NO: 35 or a complementary sequence thereof, and
- 20 variants thereof which specifically and ubiquitously anneal with strains and representatives of *Streptococcus pneumoniae*.

25

54. The method of claim 53, wherein the probe for detecting nucleic acid sequences from *Streptococcus pneumoniae* is selected from the group consisting of SEQ ID NO: 120, SEQ ID NO: 121 and a sequence complementary thereof.

30

55. A method for detecting the presence and/or amount of *Streptococcus pneumoniae* in a test sample which comprises the following steps:

- a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two

SUBSTITUTE SHEET

178

complementary strands of *Streptococcus pneumoniae* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 34 and SEQ ID NO: 35;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Streptococcus pneumoniae* in said test sample.

15

56. The method of claim 55, wherein said at least one pair of primers is selected from the group consisting of:

- a) SEQ ID NO: 78 and SEQ ID NO: 79,
- b) SEQ ID NO: 156 and SEQ ID NO: 157, and
- c) SEQ ID NO: 158 and SEQ ID NO: 159.

20

57. A method for the detection, identification and/or quantification of *Streptococcus pyogenes* directly from a test sample or from bacterial colonies, which comprises the following steps:

25

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

30

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

35

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid

SUBSTITUTE SHEET

179

which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 32, SEQ ID NO: 33, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or
5 representatives of *Streptococcus pyogenes*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label
10 being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of
15 the presence and/or amount of *Streptococcus pyogenes* in said test sample.

58. A method as defined in claim 57, wherein said probe is selected from the group consisting of:

20 1) an oligonucleotide of 12-1337 nucleotides in length which sequence is comprised in SEQ ID NO: 32 or a complementary sequence thereof,

2) an oligonucleotide of 12-1837 nucleotides in length which sequence is comprised in SEQ ID NO: 33 or a
25 complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Streptococcus pyogenes*.

30 59. A method for detecting the presence and/or amount of *Streptococcus pyogenes* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having
35 at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Streptococcus pyogenes* DNA that

SUBSTITUTE SHEET

180

contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers
5 being chosen from within one of the following sequences: SEQ ID NO: 32 and SEQ ID NO: 33;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable
10 level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Streptococcus pyogenes* in said test sample.

15 60. The method of claim 59, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 141 and SEQ ID NO: 142, and

b) SEQ ID NO: 143 and SEQ ID NO: 144.

20 61. A method for the detection, identification and/or quantification of *Enterococcus faecalis* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving
25 in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated
30 bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said
35 probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, a sequence

SUBSTITUTE SHEET

181

complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Enterococcus faecalis*, under conditions such that the nucleic acid of said probe can selectively
5 hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second
10 reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Enterococcus faecalis* in said test sample.

15

62. A method as defined in claim 61, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-1817 nucleotides in length which sequence is comprised in SEQ ID NO: 1 or a complementary
20 sequence thereof,

2) an oligonucleotide of 12-2275 nucleotides in length which sequence is comprised in SEQ ID NO: 2, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Enterococcus*
25 *faecalis*.

63. A method for detecting the presence and/or amount of *Enterococcus faecalis* in a test sample which comprises the following steps:

30 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Enterococcus faecalis* DNA that
35 contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target

SUBSTITUTE SHEET

182

sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 1 and SEQ ID NO: 2;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Enterococcus faecalis* in said test sample.

64. The method of claim 63, wherein said at least one pair of primers is selected from the group consisting of:

- a) SEQ ID NO: 38 and SEQ ID NO: 39, and
b) SEQ ID NO: 40 and SEQ ID NO: 41.

65. A method for the detection of the presence and/or amount of any bacterial species directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a universal probe which sequence is selected from the group consisting of SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130 and a sequence complementary thereof, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being

SUBSTITUTE SHEET

183

present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

- 5 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of said any bacterial species in said test sample.

- 10 66. A method for detecting the presence and/or amount of any bacterial species in a test sample which comprises the following steps:

15 a) treating said sample with an aqueous solution containing a pair of universal primers which sequence is defined in SEQ ID NO: 126 and SEQ ID NO: 127, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said any bacterial species DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said
20 strands so as to form an extension product which contains the target sequence as a template;

 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable
25 level; and

 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of said any bacterial species in said test sample.

- 30 67. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *bla_{TEM}* (TEM-1) directly from a test sample or from bacterial colonies, which comprises the following steps:

35 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

SUBSTITUTE SHEET

184

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

5 said bacterial DNA being in a substantially single stranded form;

 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group
10 consisting of SEQ ID NO: 161, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β -lactamase, under conditions such that the nucleic acid of said probe can selectively hybridize with said
15 bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said
20 probe; and

 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene TEM-1.

25

68. A method as defined in claim 67, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 161.

30 69. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *bla_{TEM}* (TEM-1) in a test sample which comprises the following steps:

 a) treating said sample with an aqueous solution
35 containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two

185

complementary strands of said bacterial antibiotic resistance gene coding for a β -lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said
5 at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 161;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence,
10 and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic
15 resistance gene TEM-1.

70. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *bla_{rob}* (ROB-1) directly from a test sample or from
20 bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

25 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single
30 stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 162, a sequence complementary
35 thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β -lactamase, under conditions such that the

SUBSTITUTE SHEET

186

nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene ROB-1.

71. A method as defined in claim 70, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 162.

72. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *bla_{rob}* (ROB-1) in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a β -lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 162;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to

SUBSTITUTE SHEET

187

β -lactam antibiotics mediated by the bacterial antibiotic resistance gene ROB-1.

73. A method for evaluating a bacterial resistance to β -lactam
5 antibiotics mediated by the bacterial antibiotic resistance
gene *bla_{shv}* (SHV-1) directly from a test sample or from
bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving
in solution the bacterial DNA of the sample or of a
10 substantially homogenous population of bacteria isolated from
this sample, or

inoculating said sample or said substantially homogenous
population of bacteria isolated from this sample on an inert
support, and lysing *in situ* said inoculated sample or isolated
15 bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single
stranded form;

b) contacting said single stranded DNA with a probe, said
probe comprising at least one single stranded nucleic acid
20 which nucleotidic sequence is selected from the group
consisting of SEQ ID NO: 163, a sequence complementary
thereof, a part thereof and a variant thereof, which
specifically anneals with said bacterial antibiotic resistance
gene coding for a β -lactamase, under conditions such that the
25 nucleic acid of said probe can selectively hybridize with said
bacterial DNA, whereby a hybridization complex is formed, said
complex being detected by labelling means, the label being
present on said probe or the label being present on a first
reactive member of said labelling means, said first reactive
30 member reacting with a second reactive member present on said
probe; and

c) detecting the presence or the intensity of said label
on said inert support or in said solution as an indication of
a bacterial r sistance to β -lactam antibiotics mediated by the
35 bacterial antibiotic resistance gene SHV-1.

SUBSTITUTE SHEET

188

74. A method as defined in claim 73, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 163.

5 75. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *bla_{SHV}* (SHV-1) in a test sample which comprises the following steps:

10 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a β -lactamase that contains a target sequence,
15 and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 163;

20 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

25 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene SHV-1.

30 76. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aadB* directly from a test sample or from bacterial colonies, which comprises the following steps:

35 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

SUBSTITUTE SHEET

189

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

5 said bacterial DNA being in a substantially single stranded form;

 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group
10 consisting of SEQ ID NO: 164, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside adenylyltransferase, under conditions such that the nucleic acid of said probe can
15 selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a
20 second reactive member present on said probe; and

 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aadB*.
25

77. A method as defined in claim 76, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 164.

30 78. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aadB* in a test sample which comprises the following steps:

 a) treating said sample with an aqueous solution
35 containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two

190

complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside adenylyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 164;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aadB*.

79. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC1* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 165, a sequence complementary thereof, a part thereof and a variant thereof, which

SUBSTITUTE SHEET

191

specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

10 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC1*.

15 80. A method as defined in claim 79, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 165.

20 81. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC1* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 165;

35 b) synthesizing an extension product of each of said primers which extension products contain the target sequence,

SUBSTITUTE SHEET

192

and amplifying said target sequence, if any, to a detectable level; and

- c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC1*.

82. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC2* directly from a test sample or from bacterial colonies, which comprises the following steps:

- a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

- b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 166, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

SUBSTITUTE SHEET

193

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC2*.

5

83. A method as defined in claim 82, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 166.

10 84. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC2* in a test sample which comprises the following steps:

15 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that
20 contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO:
25 166;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

30 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC2*.

35 85. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC3* directly from a test sample

SUBSTITUTE SHEET

194

or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 167, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC3*.

86. A method as defined in claim 85, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 167.

87. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial

SUBSTITUTE SHEET

195

antibiotic resistance gene *aacC3* in a test sample which comprises the following steps:

5 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers
10 being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 167;

15 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

20 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC3* .

25 88. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA4* directly from a test sample or from bacterial colonies, which comprises the following steps:

30 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated
35 bacteria to release the bacterial DNA,

SUBSTITUTE SHEET

196

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 168, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA4*.

89. A method as defined in claim 88, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 168.

25

90. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA4* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so

SUBSTITUTE SHEET

197

as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 168;

5 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

10 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA4*.

15 91. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *mecA* directly from a test sample or from bacterial colonies, which comprises the following steps:

20 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated
25 bacteria to release the bacterial DNA,

 said bacterial DNA being in a substantially single stranded form;

 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid
30 which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 169, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a penicillin-binding protein, under conditions
35 such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling

SUBSTITUTE SHEET

198

means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

- 5 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *mecA*.

- 10 92. A method as defined in claim 91, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 169.

- 15 93. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *mecA* in a test sample which comprises the following steps:

- 20 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a penicillin-binding protein that contains a target sequence, and the other of said primers being capable
- 25 of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 169;

- 30 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

- 35 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *mecA*.

SUBSTITUTE SHEET

199

94. A method for evaluating a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes *vanH*, *vanA* and *vanX* directly from a test sample or from bacterial colonies, which comprises the following steps:

- 5 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or
- 10 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,
- said bacterial DNA being in a substantially single stranded form;
- 15 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 170, a sequence complementary thereof, a part thereof and a variant thereof, which
- 20 specifically anneals with said bacterial antibiotic resistance genes coding for vancomycin-resistance proteins, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected
- 25 by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and
- 30 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes *vanH*, *vanA* and *vanX*.

95. A method as defined in claim 94, wherein said probe
- 35 comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 170.

SUBSTITUTE SHEET

200

96. A method for evaluating a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes *vanH*, *vanA* and *vanX* in a test sample which comprises the following steps:

- 5 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance
- 10 genes coding for vancomycin-resistance proteins that contain a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from
- 15 within the sequence defined in SEQ ID NO: 170;
- b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and
- 20 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes *vanH*, *vanA* and *vanX*.

25 97. A method for evaluating a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *sata* directly from a test sample or from bacterial colonies, which comprises the following steps:

- a) depositing and fixing on an inert support or leaving
- 30 in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or
- inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert
- 35 support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

SUBSTITUTE SHEET

201

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 173, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a streptogramin A acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *satA*.

98. A method as defined in claim 97, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 173.

25

99. A method for evaluating a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *satA* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for streptogramin A acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so

SUBSTITUTE SHEET

202

as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 173;

5 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

10 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *satA*.

15 100. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA-aphD* directly from a test sample or from bacterial colonies, which comprises the following steps:

20 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

25 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

 said bacterial DNA being in a substantially single stranded form;

30 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 174, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance
35 gene coding for an aminoglycoside acetyltransferase-phosphotransferase under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial

SUBSTITUTE SHEET

903

DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member
5 reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated
10 by the bacterial antibiotic resistance gene *aacA-aphD*.

101. A method as defined in claim 100, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 174.

15

102. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA-aphD* in a test sample which comprises the following steps:

20 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance
25 gene coding for an aminoglycoside acetyltransferase-phosphotransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one
30 pair of primers being chosen from within the sequence defined in SEQ ID NO: 174;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable
35 level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to

SUBSTITUTE SHEET

204

aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA-aphD*.

103. A method for evaluating a bacterial resistance to
5 virginiamycin mediated by the bacterial antibiotic resistance gene *vat* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving
in solution the bacterial DNA of the sample or of a
10 substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous
population of bacteria isolated from this sample on an inert
support, and lysing *in situ* said inoculated sample or isolated
15 bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single
stranded form;

b) contacting said single stranded DNA with a probe, said
probe comprising at least one single stranded nucleic acid
20 which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 175, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a virginiamycin acetyltransferase, under
25 conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said
30 labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label
on said *in situ* support or in said solution as an indication of
a bacterial resistance to virginiamycin mediated by the
35 bacterial antibiotic resistance gene *vat*.

SUBSTITUTE SHEET

205

104. A method as defined in claim 103, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 175.

- 5 105. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vat in a test sample which comprises the following steps:
- 10 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a virginiamycin acetyltransferase that contains a target sequence, and the other of said primers
- 15 being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 175;
- 20 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and
- c) detecting the presence and/or amount of said amplified
- 25 target sequence as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vat.

- 30 106. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vga directly from a test sample or from bacterial colonies, which comprises the following steps:

- a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from
- 35 this sample, or

SUBSTITUTE SHEET

206

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

5 said bacterial DNA being in a substantially single stranded form;

 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group
10 consisting of SEQ ID NO: 176, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an ATP-binding protein, under conditions such that the nucleic acid of said probe can selectively hybridize
15 with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present
20 on said probe; and

 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene *vga*.

25

107. A method as defined in claim 106, therein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 176.

30 108. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene *vga* in a test sample which comprises the following steps:

 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having
35 at least 12 nucleotides in length, on of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance

SUBSTITUTE SHEET

207

gene coding for an ATP-binding protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a
5 template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 176;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable
10 level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene *vga*.
15

109. A method for evaluating a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene *msrA* directly from a test sample or from bacterial colonies, which comprises the following steps:

20 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous
25 population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

30 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 177, a sequence complementary
there f, a part thereof and a variant thereof, which
35 specifically ann als with said bacterial antibiotic resistance gene coding for an erythromycin resistance protein under conditions such that the nucleic acid of said probe can

SUBSTITUTE SHEET

208

selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene *msrA*.

110. A method as defined in claim 109, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 177.

111. A method for evaluating a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene *msrA* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an erythromycin resistance protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 177;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to

SUBSTITUTE SHEET

209

erythromycin mediated by the bacterial antibiotic resistance gene *msrA*.

112. A method for evaluating potential bacterial resistance to
5 β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int* directly from a test sample or from bacterial colonies, which comprises the following steps:

10 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

15 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

20 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 171, a sequence complementary thereof, a part thereof and a variant thereof, which
25 specifically anneals with said bacterial antibiotic resistance gene coding for an integrase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first
30 reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

35 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int*.

SUBSTITUTE SHEET

210

113. A method as defined in claim 112, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 171.

- 5 114. A method for evaluating potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int* in a test sample which comprises the following steps:
- 10 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an integrase that contains a target sequence,
- 15 and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 171;
- 20 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and
- 25 c) detecting the presence and/or amount of said amplified target sequence as an indication of potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int*.

- 30 115. A method for evaluating potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *sul* directly from a test sample or from bacterial colonies, which comprises the following steps:

- 35 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a

SUBSTITUTE SHEET

211

substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 172, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a sulfonamide resistance protein under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *sul*.

116. A method as defined in claim 115, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 172.

117. A method for evaluating potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *sul* in a test sample which comprises the following steps:

SUBSTITUTE SHEET

212

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two
5 complementary strands of said bacterial antibiotic resistance gene coding for a sulfonamide resistance protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a
10 template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 172;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable
15 level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic
20 resistance gene *sul*.

118. A nucleic acid having the nucleotide sequence of any one of SEQ ID NOs: 1 to 37, SEQ ID NOs: 161 to 177, a part thereof and variants thereof which, when in single stranded form,
25 ubiquitously and specifically hybridize with a target bacterial DNA as a probe or as a primer.

119. An oligonucleotide having a nucleotidic sequence of any one of SEQ ID NOs: 38 to 160.

30

120. A recombinant plasmid comprising a nucleic acid as defined in claim 118.

121. A recombinant host which has been transformed by a
35 recombinant plasmid according to claim 120.

SUBSTITUTE SHEET

213

122. A recombinant host according to claim 121 wherein said host is *Escherichia coli*.

5 123. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims 9, 14, 19, 24, 29, 34, 39, 43, 47, 52, 57 and 61, comprising any combination of probes defined therein.

10 124. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims 10, 11, 15, 16, 20, 21, 25, 26, 30, 31, 35, 36, 40, 44, 48, 49, 53, 54, 58, 62 and 65, comprising any combination of oligonucleotide probes defined
15 therein.

125. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims 12, 13, 17, 18, 22, 23,
20 27, 28, 32, 33, 37, 38, 41, 42, 45, 46, 50, 51, 55, 56, 59, 60, 63, 64 and 66 comprising any combination of primers defined therein.

25 126. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes defined in any one of claims 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106 and 109 comprising any combination of probes defined therein.

30 127. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes defined in any one of claims 68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107 and 110 comprising any combination of oligonucleotide probes defined therein.

35

128. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial

SUBSTITUTE SHEET

214

resistance genes defined in any one of claims 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105, 108 and 111 comprising any combination of primers defined therein.

- 5 129. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 123, comprising any combination of the bacterial probes defined therein and any combination of the probes to the antibiotic resistance genes
10 defined in any one of SEQ ID NOs: 161 to 177 in whole or in part.

130. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the
15 bacterial species defined in claim 124, comprising any combination of the bacterial oligonucleotide probes defined therein and any combination of oligonucleotide probes that hybridize to the antibiotic resistance genes defined in any one of SEQ ID NOs: 161 to 177.

- 20 131. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 125, comprising any combination of the primers defined therein and any combination
25 of primers that anneal to the antibiotic resistance genes defined in any one of SEQ ID NOs: 161 to 177.

SUBSTITUTE SHEET